



## INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

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<b>(21) International Application Number:</b> PCT/US00/07285 <b>(22) International Filing Date:</b> 17 March 2000 (17.03.00)  <b>(30) Priority Data:</b> <table border="0"><tr><td>60/124,916</td><td>17 March 1999 (17.03.99)</td><td>US</td></tr><tr><td>60/124,808</td><td>17 March 1999 (17.03.99)</td><td>US</td></tr><tr><td>60/149,639</td><td>17 August 1999 (17.08.99)</td><td>US</td></tr><tr><td>60/157,247</td><td>1 October 1999 (01.10.99)</td><td>US</td></tr><tr><td>60/167,824</td><td>29 November 1999 (29.11.99)</td><td>US</td></tr><tr><td>60/182,711</td><td>15 February 2000 (15.02.00)</td><td>US</td></tr></table> <b>(71) Applicant:</b> ALPHAGENE, INC. [US/US]; 260 West Cummings Park, Woburn, MA 01801 (US).  <b>(72) Inventors:</b> VALENZUELA, Dario; 1081 Hill Road, Boxborough, MA 01719-1010 (US). YUAN, Olive; 292 Mystic Street, Arlington, MA 02174 (US). HOFFMAN, Heidi; 90 Houghton Mill Road, Lunenburg, MA 01462 (US). HALL, Jeff; 4 Alderwood Drive, Stratham, NH 03885 (US). RAPIEJKO, Peter; 63 Old Grafton Road, Upton, MA 01568 (US).  <b>(74) Agent:</b> SPRUNGER, Suzanne, A.; American Home Products Corporation, Patent & Trademark Dept. - 2B, One Campus Drive, Parsippany, NJ 07054 (US).		60/124,916	17 March 1999 (17.03.99)	US	60/124,808	17 March 1999 (17.03.99)	US	60/149,639	17 August 1999 (17.08.99)	US	60/157,247	1 October 1999 (01.10.99)	US	60/167,824	29 November 1999 (29.11.99)	US	60/182,711	15 February 2000 (15.02.00)	US	<b>(81) Designated States:</b> AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).  <b>Published</b> <i>With international search report.</i> <i>Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i>
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<b>(54) Title:</b> SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM																				
<b>(57) Abstract</b>  Novel polynucleotides and the proteins encoded thereby are disclosed.																				

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## SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM

5                   This application is a continuation-in-part of the following applications:

- (1)   provisional application Ser. No. 60/124,916, filed March 17, 1999;
  - (2)   provisional application Ser. No. 60/124,808, filed March 17, 1999;
  - (3)   provisional application Ser. No. 60/149,639, filed August 17, 1999;
  - (4)   provisional application Ser. No. 60/157,247, filed October 1, 1999;
  - 10 (5)   provisional application Ser. No. 60/167,824, filed November 29, 1999;
  - (6)   provisional application Ser. No. 60/182,711, filed February 15, 2000;
- all of which are incorporated by reference herein.

FIELD OF THE INVENTION

15           The present invention provides novel polynucleotides and proteins encoded by such polynucleotides, along with therapeutic, diagnostic and research utilities for these polynucleotides and proteins.

BACKGROUND OF THE INVENTION

20           Technology aimed at the discovery of protein factors (including e.g., cytokines, such as lymphokines, interferons, CSFs and interleukins) has matured rapidly over the past decade. The now routine hybridization cloning and expression cloning techniques clone novel polynucleotides "directly" in the sense that they rely on information directly related to the discovered protein (i.e., partial DNA/amino acid sequence of the protein in the case  
25 of hybridization cloning; activity of the protein in the case of expression cloning). More recent "indirect" cloning techniques such as signal sequence cloning, which isolates DNA sequences based on the presence of a now well-recognized secretory leader sequence motif, as well as various PCR-based or low stringency hybridization cloning techniques, have advanced the state of the art by making available large numbers of DNA/amino acid  
30 sequences for proteins that are known to have biological activity by virtue of their secreted nature in the case of leader sequence cloning, or by virtue of the cell or tissue source in the case of PCR-based techniques. It is to these proteins and the polynucleotides encoding them that the present invention is directed.

### SUMMARY OF THE INVENTION

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 5 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1 from nucleotide 27 to nucleotide 260;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1 from nucleotide 72 to nucleotide 260;
- 10 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vc62\_1 deposited with the ATCC under accession number 207114;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vc62\_1 deposited with the ATCC under accession number  
15 207114;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vc62\_1 deposited with the ATCC under accession number 207114;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA  
20 insert of clone vc62\_1 deposited with the ATCC under accession number 207114;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:2;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment  
25 comprising eight contiguous amino acids of SEQ ID NO:2;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 30 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:1.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:1 from nucleotide 27 to nucleotide 260; the nucleotide sequence of SEQ ID NO:1 from nucleotide 72 to nucleotide 260; the nucleotide sequence of the full-length protein coding sequence of clone vc62\_1 deposited with the ATCC under accession number 207114; or the nucleotide sequence of a mature protein coding sequence of clone vc62\_1 deposited with the ATCC under accession number 207114. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vc62\_1 deposited with the ATCC under accession number 207114. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:2, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment comprising the amino acid sequence from amino acid 34 to amino acid 43 of SEQ ID NO:2.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:1.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:1, but excluding the poly(A) tail at the 3' end of SEQ ID NO:1; and
    - (ab) the nucleotide sequence of the cDNA insert of clone vc62\_1 deposited with the ATCC under accession number 207114;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

5 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:1, but excluding the poly(A) tail at the 3' end of SEQ ID NO:1; and

10 (bb) the nucleotide sequence of the cDNA insert of clone vc62\_1 deposited with the ATCC under accession number 207114;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

15 (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:1, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:1 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:1, but excluding the poly(A) tail at the 3' end of SEQ ID NO:1. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:1 from nucleotide 27 to nucleotide 260, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:1 from nucleotide 27 to nucleotide 260, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:1 from nucleotide 27 to nucleotide 260. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:1 from nucleotide 72 to nucleotide 260, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:1 from nucleotide 72 to nucleotide 260, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:1 from nucleotide 72 to nucleotide 260.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:2;
  - 5 (b) a fragment of the amino acid sequence of SEQ ID NO:2, the fragment comprising eight contiguous amino acids of SEQ ID NO:2; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone vc62\_1 deposited with the ATCC under accession number 207114;
- the protein being substantially free from other mammalian proteins. Preferably such
- 10 protein comprises the amino acid sequence of SEQ ID NO:2. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:2, or a protein comprising a fragment of the amino acid sequence of SEQ
- 15 ID NO:2 having biological activity, the fragment comprising the amino acid sequence from amino acid 34 to amino acid 43 of SEQ ID NO:2.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID
- 20 NO:3;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:3 from nucleotide 6 to nucleotide 1325;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:3 from nucleotide 99 to nucleotide 1325;
- 25 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vp10\_1 deposited with the ATCC under accession number 207114;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vp10\_1 deposited with the ATCC under accession number
- 30 207114;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vp10\_1 deposited with the ATCC under accession number 207114;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vp10\_1 deposited with the ATCC under accession number 207114;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:4;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:4;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:3.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:3 from nucleotide 6 to nucleotide 1325; the nucleotide sequence of SEQ ID NO:3 from nucleotide 99 to nucleotide 1325; the nucleotide sequence of the full-length protein coding sequence of clone vp10\_1 deposited with the ATCC under accession number 207114; or the nucleotide sequence of a mature protein coding sequence of clone vp10\_1 deposited with the ATCC under accession number 207114. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vp10\_1 deposited with the ATCC under accession number 207114. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:4, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having

biological activity, the fragment comprising the amino acid sequence from amino acid 215 to amino acid 224 of SEQ ID NO:4.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:3.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:3, but excluding the poly(A) tail at the 3' end of SEQ ID NO:3; and

(ab) the nucleotide sequence of the cDNA insert of clone vp10\_1 deposited with the ATCC under accession number 207114;

15 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

20 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:3, but excluding the poly(A) tail at the 3' end of SEQ ID NO:3; and

(bb) the nucleotide sequence of the cDNA insert of clone vp10\_1 deposited with the ATCC under accession number 207114;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

30 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:3, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:3 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:3, but excluding the poly(A) tail at the 3' end of SEQ ID NO:3. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:3 from nucleotide 6 to nucleotide 1325, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:3 from nucleotide 6 to nucleotide 1325, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:3 from nucleotide 6 to nucleotide 1325. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:3 from nucleotide 99 to nucleotide 1325, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:3 from nucleotide 99 to nucleotide 1325, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:3 from nucleotide 99 to nucleotide 1325.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:4;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:4, the fragment comprising eight contiguous amino acids of SEQ ID NO:4; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone vp10\_1 deposited with the ATCC under accession number 207114;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:4. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:4, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment comprising the amino acid sequence from amino acid 215 to amino acid 224 of SEQ ID NO:4.



In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:5;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:5 from nucleotide 149 to nucleotide 322;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:5 from nucleotide 200 to nucleotide 322;
- 10 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vp11\_1 deposited with the ATCC under accession number 207114;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vp11\_1 deposited with the ATCC under accession number 207114;
- 15 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vp11\_1 deposited with the ATCC under accession number 207114;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vp11\_1 deposited with the ATCC under accession number 207114;
- 20 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:6;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:6;
- 25 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 30 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:5.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:5 from nucleotide 149 to nucleotide 322; the nucleotide sequence of SEQ ID NO:5 from nucleotide 200 to nucleotide 322; the nucleotide sequence of the full-length protein coding sequence of clone vp11\_1 deposited with the ATCC under accession number 207114; or the nucleotide sequence of a mature protein coding sequence of clone vp11\_1 deposited with the ATCC under accession number 207114. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vp11\_1 deposited with the ATCC under accession number 207114. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:6, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6 having biological activity, the fragment comprising the amino acid sequence from amino acid 24 to amino acid 33 of SEQ ID NO:6.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:5.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:5, but excluding the poly(A) tail at the 3' end of SEQ ID NO:5; and
    - (ab) the nucleotide sequence of the cDNA insert of clone vp11\_1 deposited with the ATCC under accession number 207114;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

5 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:5, but excluding the poly(A) tail at the 3' end of SEQ ID NO:5; and

10 (bb) the nucleotide sequence of the cDNA insert of clone vp11\_1 deposited with the ATCC under accession number 207114;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

15 (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:5, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:5 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:5, but excluding the poly(A) tail at the 3' end of SEQ ID NO:5. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:5 from nucleotide 149 to nucleotide 322, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:5 from nucleotide 149 to nucleotide 322, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:5 from nucleotide 149 to nucleotide 322. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:5 from nucleotide 200 to nucleotide 322, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:5 from nucleotide 200 to nucleotide 322, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:5 from nucleotide 200 to nucleotide 322.

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In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:6;
  - 5 (b) a fragment of the amino acid sequence of SEQ ID NO:6, the fragment comprising eight contiguous amino acids of SEQ ID NO:6; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone vp11\_1 deposited with the ATCC under accession number 207114;
- the protein being substantially free from other mammalian proteins. Preferably such
- 10 protein comprises the amino acid sequence of SEQ ID NO:6. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:6, or a protein comprising a fragment of the amino acid sequence of SEQ
- 15 ID NO:6 having biological activity, the fragment comprising the amino acid sequence from amino acid 24 to amino acid 33 of SEQ ID NO:6.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID
- 20 NO:7;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:7 from nucleotide 288 to nucleotide 629;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:7 from nucleotide 363 to nucleotide 629;
- 25 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vp13\_1 deposited with the ATCC under accession number 207114;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vp13\_1 deposited with the ATCC under accession number
- 30 207114;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vp13\_1 deposited with the ATCC under accession number 207114;

5 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vp13\_1 deposited with the ATCC under accession number 207114;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:8;

10 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:8;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

15 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:7.

20 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:7 from nucleotide 288 to nucleotide 629; the nucleotide sequence of SEQ ID NO:7 from nucleotide 363 to nucleotide 629; the nucleotide sequence of the full-length protein coding sequence of clone vp13\_1 deposited with the ATCC under accession number 207114; or the nucleotide sequence of a mature protein coding sequence of clone vp13\_1  
25 deposited with the ATCC under accession number 207114. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vp13\_1 deposited with the ATCC under accession number 207114. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of  
30 SEQ ID NO:8 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:8, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of

SEQ ID NO:8 having biological activity, the fragment comprising the amino acid sequence from amino acid 52 to amino acid 61 of SEQ ID NO:8.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:7.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

10 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:7, but excluding the poly(A) tail at the 3' end of SEQ ID NO:7; and

(ab) the nucleotide sequence of the cDNA insert of clone vp13\_1 deposited with the ATCC under accession number 207114;

15 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

20 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

25 (ba) SEQ ID NO:7, but excluding the poly(A) tail at the 3' end of SEQ ID NO:7; and

(bb) the nucleotide sequence of the cDNA insert of clone vp13\_1 deposited with the ATCC under accession number 207114;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

30 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:7, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:7 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:7, but excluding the poly(A) tail at the 3' end of SEQ ID NO:7. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:7 from nucleotide 288 to nucleotide 629, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:7 from nucleotide 288 to nucleotide 629, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:7 from nucleotide 288 to nucleotide 629. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:7 from nucleotide 363 to nucleotide 629, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:7 from nucleotide 363 to nucleotide 629, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:7 from nucleotide 363 to nucleotide 629.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:8;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:8, the fragment comprising eight contiguous amino acids of SEQ ID NO:8; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone vp13\_1 deposited with the ATCC under accession number 207114;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:8. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:8, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment comprising the amino acid sequence from amino acid 52 to amino acid 61 of SEQ ID NO:8.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:9;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:9 from nucleotide 11 to nucleotide 298;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:9 from nucleotide 149 to nucleotide 298;
- 10 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vp16\_1 deposited with the ATCC under accession number 207114;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vp16\_1 deposited with the ATCC under accession number 207114;
- 15 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vp16\_1 deposited with the ATCC under accession number 207114;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vp16\_1 deposited with the ATCC under accession number 207114;
- 20 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:10;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:10;
- 25 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 30 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and



(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:9.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:9 from nucleotide 11 to nucleotide 298; the nucleotide sequence of SEQ ID NO:9 from nucleotide 149 to nucleotide 298; the nucleotide sequence of the full-length protein coding sequence of clone vp16\_1 deposited with the ATCC under accession number 207114; or the nucleotide sequence of a mature protein coding sequence of clone vp16\_1 deposited with the ATCC under accession number 207114. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vp16\_1 deposited with the ATCC under accession number 207114. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:10, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity, the fragment comprising the amino acid sequence from amino acid 43 to amino acid 52 of SEQ ID NO:10.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:9.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:9, but excluding the poly(A) tail at the 3' end of SEQ ID NO:9; and
    - (ab) the nucleotide sequence of the cDNA insert of clone vp16\_1 deposited with the ATCC under accession number 207114;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

5 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:9, but excluding the poly(A) tail at the 3' end of SEQ ID NO:9; and

10 (bb) the nucleotide sequence of the cDNA insert of clone vp16\_1 deposited with the ATCC under accession number 207114;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

15 (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:9, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:9 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:9, but excluding the poly(A) tail at the 3' end of SEQ ID NO:9. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:9 from nucleotide 11 to nucleotide 298, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:9 from nucleotide 11 to nucleotide 298, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:9 from nucleotide 11 to nucleotide 298. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:9 from nucleotide 149 to nucleotide 298, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:9 from nucleotide 149 to nucleotide 298, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:9 from nucleotide 149 to nucleotide 298.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:10;
  - 5 (b) a fragment of the amino acid sequence of SEQ ID NO:10, the fragment comprising eight contiguous amino acids of SEQ ID NO:10; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone vp16\_1 deposited with the ATCC under accession number 207114;
- the protein being substantially free from other mammalian proteins. Preferably such
- 10 protein comprises the amino acid sequence of SEQ ID NO:10. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:10, or a protein comprising a fragment of the amino acid sequence of SEQ
- 15 ID NO:10 having biological activity, the fragment comprising the amino acid sequence from amino acid 43 to amino acid 52 of SEQ ID NO:10.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID
- 20 NO:11;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:11 from nucleotide 257 to nucleotide 607;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:11 from nucleotide 479 to nucleotide 607;
- 25 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vp21\_1 deposited with the ATCC under accession number 207114;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vp21\_1 deposited with the ATCC under accession number
- 30 207114;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vp21\_1 deposited with the ATCC under accession number 207114;

5 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vp21\_1 deposited with the ATCC under accession number 207114;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:12;

10 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:12;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

15 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:11.

20 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:11 from nucleotide 257 to nucleotide 607; the nucleotide sequence of SEQ ID NO:11 from nucleotide 479 to nucleotide 607; the nucleotide sequence of the full-length protein coding sequence of clone vp21\_1 deposited with the ATCC under accession number 207114; or the nucleotide sequence of a mature protein coding sequence of clone vp21\_1  
25 deposited with the ATCC under accession number 207114. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vp21\_1 deposited with the ATCC under accession number 207114. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of  
3.0 SEQ ID NO:12 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:12, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of

SEQ ID NO:12 having biological activity, the fragment comprising the amino acid sequence from amino acid 53 to amino acid 62 of SEQ ID NO:12.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:11.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

10

(aa) SEQ ID NO:11, but excluding the poly(A) tail at the 3' end of SEQ ID NO:11; and

(ab) the nucleotide sequence of the cDNA insert of clone vp21\_1 deposited with the ATCC under accession number 207114;

15

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

20

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

25

(ba) SEQ ID NO:11, but excluding the poly(A) tail at the 3' end of SEQ ID NO:11; and

(bb) the nucleotide sequence of the cDNA insert of clone vp21\_1 deposited with the ATCC under accession number 207114;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

30

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:11, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:11 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:11, but  
5 excluding the poly(A) tail at the 3' end of SEQ ID NO:11. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:11 from nucleotide 257 to nucleotide 607, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:11 from nucleotide 257 to nucleotide 607, to a nucleotide  
10 sequence corresponding to the 3' end of said sequence of SEQ ID NO:11 from nucleotide 257 to nucleotide 607. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:11 from nucleotide 479 to nucleotide 607, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:11 from  
15 nucleotide 479 to nucleotide 607, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:11 from nucleotide 479 to nucleotide 607.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 20 (a) the amino acid sequence of SEQ ID NO:12;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:12, the fragment comprising eight contiguous amino acids of SEQ ID NO:12; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone  
vp21\_1 deposited with the ATCC under accession number 207114;
- 25 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:12. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids  
30 of SEQ ID NO:12, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12 having biological activity, the fragment comprising the amino acid sequence from amino acid 53 to amino acid 62 of SEQ ID NO:12.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:13;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:13 from nucleotide 163 to nucleotide 477;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:13 from nucleotide 238 to nucleotide 477;
- 10 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vp22\_1 deposited with the ATCC under accession number 207114;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vp22\_1 deposited with the ATCC under accession number 207114;
- 15 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vp22\_1 deposited with the ATCC under accession number 207114;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vp22\_1 deposited with the ATCC under accession number 207114;
- 20 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:14;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:14;
- 25 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 30 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:13.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:13 from nucleotide 163 to nucleotide 477; the nucleotide sequence of SEQ ID NO:13 from nucleotide 238 to nucleotide 477; the nucleotide sequence of the full-length protein coding sequence of clone vp22\_1 deposited with the ATCC under accession number 207114; or the nucleotide sequence of a mature protein coding sequence of clone vp22\_1 deposited with the ATCC under accession number 207114. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vp22\_1 deposited with the ATCC under accession number 207114. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:14, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14 having biological activity, the fragment comprising the amino acid sequence from amino acid 47 to amino acid 56 of SEQ ID NO:14.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:13.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:13, but excluding the poly(A) tail at the 3' end of SEQ ID NO:13; and
    - (ab) the nucleotide sequence of the cDNA insert of clone vp22\_1 deposited with the ATCC under accession number 207114;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and



(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

5 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:13, but excluding the poly(A) tail at the 3' end of SEQ ID NO:13; and

10 (bb) the nucleotide sequence of the cDNA insert of clone vp22\_1 deposited with the ATCC under accession number 207114;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

15 (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:13, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:13 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:13, but  
20 excluding the poly(A) tail at the 3' end of SEQ ID NO:13. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:13 from nucleotide 163 to nucleotide 477, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:13 from nucleotide 163 to nucleotide 477, to a nucleotide  
25 sequence corresponding to the 3' end of said sequence of SEQ ID NO:13 from nucleotide 163 to nucleotide 477. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:13 from nucleotide 238 to nucleotide 477, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:13 from  
30 nucleotide 238 to nucleotide 477, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:13 from nucleotide 238 to nucleotide 477.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:14;
  - 5 (b) a fragment of the amino acid sequence of SEQ ID NO:14, the fragment comprising eight contiguous amino acids of SEQ ID NO:14; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone vp22\_1 deposited with the ATCC under accession number 207114;
- the protein being substantially free from other mammalian proteins. Preferably such
- 10 protein comprises the amino acid sequence of SEQ ID NO:14. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:14, or a protein comprising a fragment of the amino acid sequence of SEQ
- 15 ID NO:14 having biological activity, the fragment comprising the amino acid sequence from amino acid 47 to amino acid 56 of SEQ ID NO:14.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID
- 20 NO:15;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:15 from nucleotide 58 to nucleotide 624;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:15 from nucleotide 106 to nucleotide 624;
- 25 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vq2\_1 deposited with the ATCC under accession number 207114;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vq2\_1 deposited with the ATCC under accession number
- 30 207114;

- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vq2\_1 deposited with the ATCC under accession number 207114;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vq2\_1 deposited with the ATCC under accession number 207114;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:16;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:16;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:15.
- Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:15 from nucleotide 58 to nucleotide 624; the nucleotide sequence of SEQ ID NO:15 from nucleotide 106 to nucleotide 624; the nucleotide sequence of the full-length protein coding sequence of clone vq2\_1 deposited with the ATCC under accession number 207114; or the nucleotide sequence of a mature protein coding sequence of clone vq2\_1 deposited with the ATCC under accession number 207114. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vq2\_1 deposited with the ATCC under accession number 207114. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:16, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of

SEQ ID NO:16 having biological activity, the fragment comprising the amino acid sequence from amino acid 89 to amino acid 98 of SEQ ID NO:16.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:15.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

10

(aa) SEQ ID NO:15, but excluding the poly(A) tail at the 3' end of SEQ ID NO:15; and

(ab) the nucleotide sequence of the cDNA insert of clone vq2\_1 deposited with the ATCC under accession number 207114;

15

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

20

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

25

(ba) SEQ ID NO:15, but excluding the poly(A) tail at the 3' end of SEQ ID NO:15; and

(bb) the nucleotide sequence of the cDNA insert of clone vq2\_1 deposited with the ATCC under accession number 207114;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

30

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:15, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:15 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:15, but  
5 excluding the poly(A) tail at the 3' end of SEQ ID NO:15. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:15 from nucleotide 58 to nucleotide 624, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:15 from nucleotide 58 to nucleotide 624, to a nucleotide  
10 sequence corresponding to the 3' end of said sequence of SEQ ID NO:15 from nucleotide 58 to nucleotide 624. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:15 from nucleotide 106 to nucleotide 624, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:15 from  
15 nucleotide 106 to nucleotide 624, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:15 from nucleotide 106 to nucleotide 624.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 20 (a) the amino acid sequence of SEQ ID NO:16;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:16, the fragment comprising eight contiguous amino acids of SEQ ID NO:16; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone  
vq2\_1 deposited with the ATCC under accession number 207114;
- 25 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:16. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids  
30 of SEQ ID NO:16, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment comprising the amino acid sequence from amino acid 89 to amino acid 98 of SEQ ID NO:16.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:17;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:17 from nucleotide 773 to nucleotide 1090;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:17 from nucleotide 842 to nucleotide 1090;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vq3\_1 deposited with the ATCC under  
10 accession number 207114;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vq3\_1 deposited with the ATCC under accession number 207114;
- 15 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vq3\_1 deposited with the ATCC under accession number 207114;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vq3\_1 deposited with the ATCC under accession number 207114;
- 20 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:18;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:18;
- 25 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any  
30 one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:17.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:17 from nucleotide 773 to nucleotide 1090; the nucleotide sequence of SEQ ID NO:17 from nucleotide 842 to nucleotide 1090; the nucleotide sequence of the full-length protein coding sequence of clone vq3\_1 deposited with the ATCC under accession number 207114; or the nucleotide sequence of a mature protein coding sequence of clone vq3\_1 deposited with the ATCC under accession number 207114. In other preferred  
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embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vq3\_1 deposited with the ATCC under accession number 207114. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:18, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18 having biological activity, the fragment comprising the amino acid sequence from amino acid 48 to amino acid 57 of SEQ ID NO:18.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:17.  
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Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize  
25 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:17, but excluding the poly(A) tail at the 3' end of SEQ ID NO:17; and
    - (ab) the nucleotide sequence of the cDNA insert of clone  
30 vq3\_1 deposited with the ATCC under accession number 207114;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

5 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:17, but excluding the poly(A) tail at the 3' end of SEQ ID NO:17; and

10 (bb) the nucleotide sequence of the cDNA insert of clone vq3\_1 deposited with the ATCC under accession number 207114;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

15 (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:17, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:17 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:17, but  
20 excluding the poly(A) tail at the 3' end of SEQ ID NO:17. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:17 from nucleotide 773 to nucleotide 1090, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:17 from nucleotide 773 to nucleotide 1090, to a nucleotide  
25 sequence corresponding to the 3' end of said sequence of SEQ ID NO:17 from nucleotide 773 to nucleotide 1090. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:17 from nucleotide 842 to nucleotide 1090, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:17 from  
30 nucleotide 842 to nucleotide 1090, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:17 from nucleotide 842 to nucleotide 1090.



In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:18;
  - 5 (b) a fragment of the amino acid sequence of SEQ ID NO:18, the fragment comprising eight contiguous amino acids of SEQ ID NO:18; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone vq3\_1 deposited with the ATCC under accession number 207114;
- the protein being substantially free from other mammalian proteins. Preferably such
- 10 protein comprises the amino acid sequence of SEQ ID NO:18. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:18, or a protein comprising a fragment of the amino acid sequence of SEQ
- 15 ID NO:18 having biological activity, the fragment comprising the amino acid sequence from amino acid 48 to amino acid 57 of SEQ ID NO:18.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID
- 20 NO:19;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:19 from nucleotide 96 to nucleotide 275;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:19 from nucleotide 159 to nucleotide 275;
- 25 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vq5\_1 deposited with the ATCC under accession number 207114;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vq5\_1 deposited with the ATCC under accession number
- 30 207114;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vq5\_1 deposited with the ATCC under accession number 207114;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vq5\_1 deposited with the ATCC under accession number 207114;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:20;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:20;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:19.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:19 from nucleotide 96 to nucleotide 275; the nucleotide sequence of SEQ ID NO:19 from nucleotide 159 to nucleotide 275; the nucleotide sequence of the full-length protein coding sequence of clone vq5\_1 deposited with the ATCC under accession number 207114; or the nucleotide sequence of a mature protein coding sequence of clone vq5\_1 deposited with the ATCC under accession number 207114. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vq5\_1 deposited with the ATCC under accession number 207114. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:20, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of

SEQ ID NO:20 having biological activity, the fragment comprising the amino acid sequence from amino acid 25 to amino acid 34 of SEQ ID NO:20.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:19.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

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(aa) SEQ ID NO:19, but excluding the poly(A) tail at the 3' end of SEQ ID NO:19; and

(ab) the nucleotide sequence of the cDNA insert of clone vq5\_1 deposited with the ATCC under accession number 207114;

15

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

20

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

25

(ba) SEQ ID NO:19, but excluding the poly(A) tail at the 3' end of SEQ ID NO:19; and

(bb) the nucleotide sequence of the cDNA insert of clone vq5\_1 deposited with the ATCC under accession number 207114;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

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(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:19, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:19 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:19, but excluding the poly(A) tail at the 3' end of SEQ ID NO:19. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:19 from nucleotide 96 to nucleotide 275, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:19 from nucleotide 96 to nucleotide 275, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:19 from nucleotide 96 to nucleotide 275. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:19 from nucleotide 159 to nucleotide 275, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:19 from nucleotide 159 to nucleotide 275, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:19 from nucleotide 159 to nucleotide 275.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:20;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:20, the fragment comprising eight contiguous amino acids of SEQ ID NO:20; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone vq5\_1 deposited with the ATCC under accession number 207114;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:20. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:20, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20 having biological activity, the fragment comprising the amino acid sequence from amino acid 25 to amino acid 34 of SEQ ID NO:20.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:21;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:21 from nucleotide 176 to nucleotide 340;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:21 from nucleotide 230 to nucleotide 340;
- 10 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vq6\_1 deposited with the ATCC under accession number 207114;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vq6\_1 deposited with the ATCC under accession number 207114;
- 15 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vq6\_1 deposited with the ATCC under accession number 207114;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vq6\_1 deposited with the ATCC under accession number 207114;
- 20 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:22;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:22;
- 25 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 30 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:21.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:21 from nucleotide 176 to nucleotide 340; the nucleotide sequence of SEQ ID NO:21 from nucleotide 230 to nucleotide 340; the nucleotide sequence of the full-length protein coding sequence of clone vq6\_1 deposited with the ATCC under accession number 207114; or the nucleotide sequence of a mature protein coding sequence of clone vq6\_1 deposited with the ATCC under accession number 207114. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vq6\_1 deposited with the ATCC under accession number 207114. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:22, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22 having biological activity, the fragment comprising the amino acid sequence from amino acid 22 to amino acid 31 of SEQ ID NO:22.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:21.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:21, but excluding the poly(A) tail at the 3' end of SEQ ID NO:21; and
    - (ab) the nucleotide sequence of the cDNA insert of clone vq6\_1 deposited with the ATCC under accession number 207114;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

5 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:21, but excluding the poly(A) tail at the 3' end of SEQ ID NO:21; and

10 (bb) the nucleotide sequence of the cDNA insert of clone vq6\_1 deposited with the ATCC under accession number 207114;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

15 (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:21, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:21 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:21, but  
20 excluding the poly(A) tail at the 3' end of SEQ ID NO:21. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:21 from nucleotide 176 to nucleotide 340, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:21 from nucleotide 176 to nucleotide 340, to a nucleotide  
25 sequence corresponding to the 3' end of said sequence of SEQ ID NO:21 from nucleotide 176 to nucleotide 340. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:21 from nucleotide 230 to nucleotide 340, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:21 from  
30 nucleotide 230 to nucleotide 340, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:21 from nucleotide 230 to nucleotide 340.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:22;
  - 5 (b) a fragment of the amino acid sequence of SEQ ID NO:22, the fragment comprising eight contiguous amino acids of SEQ ID NO:22; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone vq6\_1 deposited with the ATCC under accession number 207114;
- the protein being substantially free from other mammalian proteins. Preferably such
- 10 protein comprises the amino acid sequence of SEQ ID NO:22. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:22, or a protein comprising a fragment of the amino acid sequence of SEQ
- 15 ID NO:22 having biological activity, the fragment comprising the amino acid sequence from amino acid 22 to amino acid 31 of SEQ ID NO:22.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID
- 20 NO:23;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:23 from nucleotide 29 to nucleotide 1111;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:23 from nucleotide 167 to nucleotide 1111;
- 25 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vr1\_1 deposited with the ATCC under accession number 207114;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vr1\_1 deposited with the ATCC under accession number
- 30 207114;



(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vr1\_1 deposited with the ATCC under accession number 207114;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vr1\_1 deposited with the ATCC under accession number 207114;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:24;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:24;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:23.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:23 from nucleotide 29 to nucleotide 1111; the nucleotide sequence of SEQ ID NO:23 from nucleotide 167 to nucleotide 1111; the nucleotide sequence of the full-length protein coding sequence of clone vr1\_1 deposited with the ATCC under accession number 207114; or the nucleotide sequence of a mature protein coding sequence of clone vr1\_1 deposited with the ATCC under accession number 207114. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vr1\_1 deposited with the ATCC under accession number 207114.

In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:24, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of

SEQ ID NO:24 having biological activity, the fragment comprising the amino acid sequence from amino acid 175 to amino acid 184 of SEQ ID NO:24.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:23.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

10 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:23, but excluding the poly(A) tail at the 3' end of SEQ ID NO:23; and

(ab) the nucleotide sequence of the cDNA insert of clone vr1\_1 deposited with the ATCC under accession number 207114;

15 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

20 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

25 (ba) SEQ ID NO:23, but excluding the poly(A) tail at the 3' end of SEQ ID NO:23; and

(bb) the nucleotide sequence of the cDNA insert of clone vr1\_1 deposited with the ATCC under accession number 207114;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

30 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:23, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:23 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:23, but  
5 excluding the poly(A) tail at the 3' end of SEQ ID NO:23. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:23 from nucleotide 29 to nucleotide 1111, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:23 from nucleotide 29 to nucleotide 1111, to a nucleotide  
10 sequence corresponding to the 3' end of said sequence of SEQ ID NO:23 from nucleotide 29 to nucleotide 1111. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:23 from nucleotide 167 to nucleotide 1111, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:23 from  
15 nucleotide 167 to nucleotide 1111, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:23 from nucleotide 167 to nucleotide 1111.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 20 (a) the amino acid sequence of SEQ ID NO:24;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:24, the fragment comprising eight contiguous amino acids of SEQ ID NO:24; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone  
vr1\_1 deposited with the ATCC under accession number 207114;
- 25 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:24. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids  
30 of SEQ ID NO:24, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24 having biological activity, the fragment comprising the amino acid sequence from amino acid 175 to amino acid 184 of SEQ ID NO:24.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:25;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:25 from nucleotide 13 to nucleotide 513;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vc63\_1 deposited with the ATCC under accession number 207115;
- 10 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vc63\_1 deposited with the ATCC under accession number 207115;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vc63\_1 deposited with the ATCC under  
15 accession number 207115;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vc63\_1 deposited with the ATCC under accession number 207115;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:26;
- 20 (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:26;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- 25 (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any  
30 one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:25.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:25 from nucleotide 13 to nucleotide 513; the nucleotide sequence of the full-length protein coding sequence of clone vc63\_1 deposited with the ATCC under accession number 207115; or the nucleotide sequence of a mature protein coding sequence of clone  
5 vc63\_1 deposited with the ATCC under accession number 207115. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vc63\_1 deposited with the ATCC under accession number 207115. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of  
10 SEQ ID NO:26 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:26, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26 having biological activity, the fragment comprising the amino acid sequence from amino acid 78 to amino acid 87 of SEQ ID NO:26.

15 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:25.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - 20 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:25, but excluding the poly(A) tail at the 3' end of SEQ ID NO:25; and
    - 25 (ab) the nucleotide sequence of the cDNA insert of clone vc63\_1 deposited with the ATCC under accession number 207115;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
  - (iii) isolating the DNA polynucleotides detected with the  
30 probe(s);

and

- (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- 5 (ba) SEQ ID NO:25, but excluding the poly(A) tail at the 3' end of SEQ ID NO:25; and
- (bb) the nucleotide sequence of the cDNA insert of clone vc63\_1 deposited with the ATCC under accession number 207115;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- 10 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:25, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID

15 NO:25 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:25, but excluding the poly(A) tail at the 3' end of SEQ ID NO:25. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:25 from nucleotide 13 to nucleotide 513, and extending contiguously from a nucleotide sequence corresponding to the 5' end

20 of said sequence of SEQ ID NO:25 from nucleotide 13 to nucleotide 513, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:25 from nucleotide 13 to nucleotide 513.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group

25 consisting of:

- (a) the amino acid sequence of SEQ ID NO:26;
- (b) a fragment of the amino acid sequence of SEQ ID NO:26, the fragment comprising eight contiguous amino acids of SEQ ID NO:26; and
- (c) the amino acid sequence encoded by the cDNA insert of clone
- 30 vc63\_1 deposited with the ATCC under accession number 207115;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:26. In further preferred

embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:26, or a protein comprising a fragment of the amino acid sequence of SEQ  
5 ID NO:26 having biological activity, the fragment comprising the amino acid sequence from amino acid 78 to amino acid 87 of SEQ ID NO:26.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 10 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:27;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:27 from nucleotide 79 to nucleotide 345;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:27 from nucleotide 130 to nucleotide 345;
- 15 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vb25\_1 deposited with the ATCC under accession number PTA-362;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vb25\_1 deposited with the ATCC under accession number  
20 PTA-362;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vb25\_1 deposited with the ATCC under accession number PTA-362;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA  
25 insert of clone vb25\_1 deposited with the ATCC under accession number PTA-362;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:28;
- 30 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:28;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

5 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:27.

10 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:27 from nucleotide 79 to nucleotide 345; the nucleotide sequence of SEQ ID NO:27 from nucleotide 130 to nucleotide 345; the nucleotide sequence of the full-length protein coding sequence of clone vb25\_1 deposited with the ATCC under accession number PTA-362; or the nucleotide sequence of a mature protein coding sequence of clone vb25\_1  
15 deposited with the ATCC under accession number PTA-362. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vb25\_1 deposited with the ATCC under accession number PTA-362. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28  
20 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:28, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment comprising the amino acid sequence from amino acid 39 to amino acid 48 of SEQ ID NO:28.

25 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:27.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

30 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:



(aa) SEQ ID NO:27, but excluding the poly(A) tail at the 3' end of SEQ ID NO:27; and

(ab) the nucleotide sequence of the cDNA insert of clone vb25\_1 deposited with the ATCC under accession number PTA-362;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

10 and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

15 (ba) SEQ ID NO:27, but excluding the poly(A) tail at the 3' end of SEQ ID NO:27; and

(bb) the nucleotide sequence of the cDNA insert of clone vb25\_1 deposited with the ATCC under accession number PTA-362;

20 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a  
25 nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:27, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:27 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:27, but excluding the poly(A) tail at the 3' end of SEQ ID NO:27. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence  
30 corresponding to the cDNA sequence of SEQ ID NO:27 from nucleotide 79 to nucleotide 345, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:27 from nucleotide 79 to nucleotide 345, to a nucleotide

sequence corresponding to the 3' end of said sequence of SEQ ID NO:27 from nucleotide 79 to nucleotide 345. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:27 from nucleotide 130 to nucleotide 345, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:27 from nucleotide 130 to nucleotide 345, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:27 from nucleotide 130 to nucleotide 345.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:28;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:28, the fragment comprising eight contiguous amino acids of SEQ ID NO:28; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone vb25\_1 deposited with the ATCC under accession number PTA-362;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:28. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:28, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment comprising the amino acid sequence from amino acid 39 to amino acid 48 of SEQ ID NO:28.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:29;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:29 from nucleotide 72 to nucleotide 236;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:29 from nucleotide 150 to nucleotide 236;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vb27\_1 deposited with the ATCC under accession number PTA-362;

5 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vb27\_1 deposited with the ATCC under accession number PTA-362;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vb27\_1 deposited with the ATCC under accession number PTA-362;

10 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vb27\_1 deposited with the ATCC under accession number PTA-362;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:30;

15 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:30;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

20 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

25 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:29.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:29 from nucleotide 72 to nucleotide 236; the nucleotide sequence of SEQ ID NO:29 from nucleotide 150 to nucleotide 236; the nucleotide sequence of the full-length protein coding sequence of clone vb27\_1 deposited with the ATCC under accession number PTA-362; or the nucleotide sequence of a mature protein coding sequence of clone vb27\_1 deposited with the ATCC under accession number PTA-362. In other preferred

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embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vb27\_1 deposited with the ATCC under accession number PTA-362. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30  
5 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:30, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment comprising the amino acid sequence from amino acid 22 to amino acid 31 of SEQ ID NO:30.

10 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:29.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - 15 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:29, but excluding the poly(A) tail at the 3' end of SEQ ID NO:29; and
    - 20 (ab) the nucleotide sequence of the cDNA insert of clone vb27\_1 deposited with the ATCC under accession number PTA-362;
    - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
    - 25 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
  - (i) preparing one or more polynucleotide primers that hybridize  
30 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- (ba) SEQ ID NO:29, but excluding the poly(A) tail at the 3' end of SEQ ID NO:29; and
- (bb) the nucleotide sequence of the cDNA insert of clone vb27\_1 deposited with the ATCC under accession number PTA-362;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).
- 10 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:29, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:29 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:29, but excluding the poly(A) tail at the 3' end of SEQ ID NO:29. Also preferably the
- 15 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:29 from nucleotide 72 to nucleotide 236, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:29 from nucleotide 72 to nucleotide 236, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:29 from nucleotide
- 20 72 to nucleotide 236. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:29 from nucleotide 150 to nucleotide 236, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:29 from nucleotide 150 to nucleotide 236, to a nucleotide sequence corresponding to the 3' end of
- 25 said sequence of SEQ ID NO:29 from nucleotide 150 to nucleotide 236.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:30;
- 30 (b) a fragment of the amino acid sequence of SEQ ID NO:30, the fragment comprising eight contiguous amino acids of SEQ ID NO:30; and

(c) the amino acid sequence encoded by the cDNA insert of clone vb27\_1 deposited with the ATCC under accession number PTA-362; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:30. In further preferred  
5 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:30, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment comprising the amino acid sequence  
10 from amino acid 22 to amino acid 31 of SEQ ID NO:30.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:31;
- 15 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:31 from nucleotide 135 to nucleotide 884;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:31 from nucleotide 183 to nucleotide 884;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vb28\_1 deposited with the ATCC under  
20 accession number PTA-362;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vb28\_1 deposited with the ATCC under accession number PTA-362;
- 25 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vb28\_1 deposited with the ATCC under accession number PTA-362;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vb28\_1 deposited with the ATCC under accession number PTA-  
30 362;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:32;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:32;

5 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

10 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:31.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:31 from nucleotide 135 to nucleotide 884; the nucleotide sequence of SEQ ID NO:31  
15 from nucleotide 183 to nucleotide 884; the nucleotide sequence of the full-length protein coding sequence of clone vb28\_1 deposited with the ATCC under accession number PTA-362; or the nucleotide sequence of a mature protein coding sequence of clone vb28\_1 deposited with the ATCC under accession number PTA-362. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by  
20 the cDNA insert of clone vb28\_1 deposited with the ATCC under accession number PTA-362. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:32, or a  
25 polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32 having biological activity, the fragment comprising the amino acid sequence from amino acid 120 to amino acid 129 of SEQ ID NO:32.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:31.

30 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (aa) SEQ ID NO:31, but excluding the poly(A) tail at the 3' end of SEQ ID NO:31; and

(ab) the nucleotide sequence of the cDNA insert of clone vb28\_1 deposited with the ATCC under accession number PTA-362;

10 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

15 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:31, but excluding the poly(A) tail at the 3' end of SEQ ID NO:31; and

20 (bb) the nucleotide sequence of the cDNA insert of clone vb28\_1 deposited with the ATCC under accession number PTA-362;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

25 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:31, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID  
30 NO:31 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:31, but excluding the poly(A) tail at the 3' end of SEQ ID NO:31. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence



corresponding to the cDNA sequence of SEQ ID NO:31 from nucleotide 135 to nucleotide 884, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:31 from nucleotide 135 to nucleotide 884, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:31 from nucleotide 135 to nucleotide 884. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:31 from nucleotide 183 to nucleotide 884, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:31 from nucleotide 183 to nucleotide 884, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:31 from nucleotide 183 to nucleotide 884.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:32;
- (b) a fragment of the amino acid sequence of SEQ ID NO:32, the fragment comprising eight contiguous amino acids of SEQ ID NO:32; and
- (c) the amino acid sequence encoded by the cDNA insert of clone vb28\_1 deposited with the ATCC under accession number PTA-362;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:32. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:32, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32 having biological activity, the fragment comprising the amino acid sequence from amino acid 120 to amino acid 129 of SEQ ID NO:32.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:33;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:33 from nucleotide 42 to nucleotide 206;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:33 from nucleotide 111 to nucleotide 206;

5 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vb29\_1 deposited with the ATCC under accession number PTA-362;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vb29\_1 deposited with the ATCC under accession number PTA-362;

10 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vb29\_1 deposited with the ATCC under accession number PTA-362;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vb29\_1 deposited with the ATCC under accession number PTA-362;

15 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:34;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:34;

20 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

25 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:33.

30 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:33 from nucleotide 42 to nucleotide 206; the nucleotide sequence of SEQ ID NO:33 from nucleotide 111 to nucleotide 206; the nucleotide sequence of the full-length protein coding sequence of clone vb29\_1 deposited with the ATCC under accession number PTA-

362; or the nucleotide sequence of a mature protein coding sequence of clone vb29\_1 deposited with the ATCC under accession number PTA-362. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vb29\_1 deposited with the ATCC under accession number PTA-362. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:34, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34 having biological activity, the fragment comprising the amino acid sequence from amino acid 22 to amino acid 31 of SEQ ID NO:34.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:33.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:33, but excluding the poly(A) tail at the 3' end of SEQ ID NO:33; and

(ab) the nucleotide sequence of the cDNA insert of clone vb29\_1 deposited with the ATCC under accession number PTA-362;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (ba) SEQ ID NO:33, but excluding the poly(A) tail at the 3' end of SEQ ID NO:33; and

(bb) the nucleotide sequence of the cDNA insert of clone vb29\_1 deposited with the ATCC under accession number PTA-362;

10 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:33, and  
15 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:33 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:33, but excluding the poly(A) tail at the 3' end of SEQ ID NO:33. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:33 from nucleotide 42 to nucleotide  
20 206, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:33 from nucleotide 42 to nucleotide 206, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:33 from nucleotide 42 to nucleotide 206. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID  
25 NO:33 from nucleotide 111 to nucleotide 206, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:33 from nucleotide 111 to nucleotide 206, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:33 from nucleotide 111 to nucleotide 206.

In other embodiments, the present invention provides a composition comprising  
30 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:34;

- (b) a fragment of the amino acid sequence of SEQ ID NO:34, the fragment comprising eight contiguous amino acids of SEQ ID NO:34; and
- (c) the amino acid sequence encoded by the cDNA insert of clone vb29\_1 deposited with the ATCC under accession number PTA-362;
- 5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:34. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 10 of SEQ ID NO:34, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34 having biological activity, the fragment comprising the amino acid sequence from amino acid 22 to amino acid 31 of SEQ ID NO:34.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 15 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:35;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:35 from nucleotide 17 to nucleotide 253;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
- 20 NO:35 from nucleotide 98 to nucleotide 253;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vb30\_1 deposited with the ATCC under accession number PTA-362;
- (e) a polynucleotide encoding the full-length protein encoded by the
- 25 cDNA insert of clone vb30\_1 deposited with the ATCC under accession number PTA-362;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vb30\_1 deposited with the ATCC under accession number PTA-362;
- 30 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vb30\_1 deposited with the ATCC under accession number PTA-362;

- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:36;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:36;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:35.
- Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:35 from nucleotide 17 to nucleotide 253; the nucleotide sequence of SEQ ID NO:35 from nucleotide 98 to nucleotide 253; the nucleotide sequence of the full-length protein coding sequence of clone vb30\_1 deposited with the ATCC under accession number PTA-362; or the nucleotide sequence of a mature protein coding sequence of clone vb30\_1 deposited with the ATCC under accession number PTA-362. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vb30\_1 deposited with the ATCC under accession number PTA-362. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:36, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36 having biological activity, the fragment comprising the amino acid sequence from amino acid 34 to amino acid 43 of SEQ ID NO:36.
- Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:35.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:35, but excluding the poly(A) tail at the 3' end of SEQ ID NO:35; and

(ab) the nucleotide sequence of the cDNA insert of clone vb30\_1 deposited with the ATCC under accession number PTA-362;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:35, but excluding the poly(A) tail at the 3' end of SEQ ID NO:35; and

(bb) the nucleotide sequence of the cDNA insert of clone vb30\_1 deposited with the ATCC under accession number PTA-362;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:35, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID

NO:35 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:35 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:35. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:35 from nucleotide 17 to nucleotide 5 253, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:35 from nucleotide 17 to nucleotide 253, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:35 from nucleotide 17 to nucleotide 253. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID 10 NO:35 from nucleotide 98 to nucleotide 253, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:35 from nucleotide 98 to nucleotide 253, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:35 from nucleotide 98 to nucleotide 253.

In other embodiments, the present invention provides a composition comprising 15 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:36;
- (b) a fragment of the amino acid sequence of SEQ ID NO:36, the fragment comprising eight contiguous amino acids of SEQ ID NO:36; and
- 20 (c) the amino acid sequence encoded by the cDNA insert of clone vb30\_1 deposited with the ATCC under accession number PTA-362;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:36. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino 25 acid sequence of SEQ ID NO:36 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:36, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36 having biological activity, the fragment comprising the amino acid sequence from amino acid 34 to amino acid 43 of SEQ ID NO:36.

30 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:



- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:37;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:37 from nucleotide 68 to nucleotide 424;
- 5 (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vc67\_1 deposited with the ATCC under accession number PTA-362;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vc67\_1 deposited with the ATCC under accession number  
10 PTA-362;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vc67\_1 deposited with the ATCC under accession number PTA-362;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA  
15 insert of clone vc67\_1 deposited with the ATCC under accession number PTA-362;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:38;
- (h) a polynucleotide encoding a protein comprising a fragment of the  
20 amino acid sequence of SEQ ID NO:38 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:38;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein  
25 of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least  
30 25% of the length of SEQ ID NO:37.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:37 from nucleotide 68 to nucleotide 424; the nucleotide sequence of the full-length

protein coding sequence of clone vc67\_1 deposited with the ATCC under accession number PTA-362; or the nucleotide sequence of a mature protein coding sequence of clone vc67\_1 deposited with the ATCC under accession number PTA-362. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vc67\_1 deposited with the ATCC under accession number PTA-362. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:38, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38 having biological activity, the fragment comprising the amino acid sequence from amino acid 54 to amino acid 63 of SEQ ID NO:38.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:37.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:37, but excluding the poly(A) tail at the 3' end of SEQ ID NO:37; and

(ab) the nucleotide sequence of the cDNA insert of clone vc67\_1 deposited with the ATCC under accession number PTA-362;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (ba) SEQ ID NO:37, but excluding the poly(A) tail at the 3' end of SEQ ID NO:37; and

(bb) the nucleotide sequence of the cDNA insert of clone vc67\_1 deposited with the ATCC under accession number PTA-362;

10 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:37, and  
15 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:37 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:37, but excluding the poly(A) tail at the 3' end of SEQ ID NO:37. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:37 from nucleotide  
20 424, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:37 from nucleotide 68 to nucleotide 424, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:37 from nucleotide 68 to nucleotide 424.

In other embodiments, the present invention provides a composition comprising  
25 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:38;

(b) a fragment of the amino acid sequence of SEQ ID NO:38, the fragment comprising eight contiguous amino acids of SEQ ID NO:38; and

30 (c) the amino acid sequence encoded by the cDNA insert of clone vc67\_1 deposited with the ATCC under accession number PTA-362;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:38. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38 having biological activity, the fragment preferably  
5 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:38, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38 having biological activity, the fragment comprising the amino acid sequence from amino acid 54 to amino acid 63 of SEQ ID NO:38.

In one embodiment, the present invention provides a composition comprising an  
10 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:39;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:39 from nucleotide 103 to nucleotide 261;
- 15 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:39 from nucleotide 154 to nucleotide 261;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vf4\_1 deposited with the ATCC under accession number PTA-362;
- 20 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vf4\_1 deposited with the ATCC under accession number PTA-362;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vf4\_1 deposited with the ATCC under accession  
25 number PTA-362;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vf4\_1 deposited with the ATCC under accession number PTA-362;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:40;
- 30 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:40;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

5 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:39.

10 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:39 from nucleotide 103 to nucleotide 261; the nucleotide sequence of SEQ ID NO:39 from nucleotide 154 to nucleotide 261; the nucleotide sequence of the full-length protein coding sequence of clone vf4\_1 deposited with the ATCC under accession number PTA-362; or the nucleotide sequence of a mature protein coding sequence of clone vf4\_1  
15 deposited with the ATCC under accession number PTA-362. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vf4\_1 deposited with the ATCC under accession number PTA-362. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40  
20 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:40, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment comprising the amino acid sequence from amino acid 21 to amino acid 30 of SEQ ID NO:40.

25 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:39.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

30 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- (aa) SEQ ID NO:39, but excluding the poly(A) tail at the 3' end of SEQ ID NO:39; and
- (ab) the nucleotide sequence of the cDNA insert of clone vf4\_1 deposited with the ATCC under accession number PTA-362;
- 5 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- 10 (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:39, but excluding the poly(A) tail at the 15 3' end of SEQ ID NO:39; and
- (bb) the nucleotide sequence of the cDNA insert of clone vf4\_1 deposited with the ATCC under accession number PTA-362;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- 20 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:39, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID

25 NO:39 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:39, but excluding the poly(A) tail at the 3' end of SEQ ID NO:39. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:39 from nucleotide 103 to nucleotide 261, and extending contiguously from a nucleotide sequence corresponding to the 5' end

30 of said sequence of SEQ ID NO:39 from nucleotide 103 to nucleotide 261, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:39 from nucleotide 103 to nucleotide 261. Also preferably the polynucleotide isolated according to the above

process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:39 from nucleotide 154 to nucleotide 261, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:39 from nucleotide 154 to nucleotide 261, to a nucleotide sequence corresponding to the 3' end of  
5 said sequence of SEQ ID NO:39 from nucleotide 154 to nucleotide 261.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:40;
  - 10 (b) a fragment of the amino acid sequence of SEQ ID NO:40, the fragment comprising eight contiguous amino acids of SEQ ID NO:40; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone vf4\_1 deposited with the ATCC under accession number PTA-362;
- the protein being substantially free from other mammalian proteins. Preferably such  
15 protein comprises the amino acid sequence of SEQ ID NO:40. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:40, or a protein comprising a fragment of the amino acid sequence of SEQ  
20 ID NO:40 having biological activity, the fragment comprising the amino acid sequence from amino acid 21 to amino acid 30 of SEQ ID NO:40.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID  
25 NO:41;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:41 from nucleotide 1575 to nucleotide 3038;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:41 from nucleotide 1650 to nucleotide 3038;
- 30 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vg3\_1 deposited with the ATCC under accession number PTA-362;

- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vg3\_1 deposited with the ATCC under accession number PTA-362;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vg3\_1 deposited with the ATCC under accession number PTA-362;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vg3\_1 deposited with the ATCC under accession number PTA-362;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:42;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:42;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:41.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:41 from nucleotide 1575 to nucleotide 3038; the nucleotide sequence of SEQ ID NO:41 from nucleotide 1650 to nucleotide 3038; the nucleotide sequence of the full-length protein coding sequence of clone vg3\_1 deposited with the ATCC under accession number PTA-362; or the nucleotide sequence of a mature protein coding sequence of clone vg3\_1 deposited with the ATCC under accession number PTA-362. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vg3\_1 deposited with the ATCC under accession number PTA-362. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42



having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:42, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment comprising the amino acid  
5 sequence from amino acid 239 to amino acid 248 of SEQ ID NO:42.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:41.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 10 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:41, but excluding the poly(A) tail at the  
15 3' end of SEQ ID NO:41; and
    - (ab) the nucleotide sequence of the cDNA insert of clone vg3\_1 deposited with the ATCC under accession number PTA-362;
    - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
  - 20 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that hybridize  
25 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (ba) SEQ ID NO:41, but excluding the poly(A) tail at the 3' end of SEQ ID NO:41; and
    - (bb) the nucleotide sequence of the cDNA insert of clone  
30 vg3\_1 deposited with the ATCC under accession number PTA-362;
    - (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:41, and  
5 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:41 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:41, but excluding the poly(A) tail at the 3' end of SEQ ID NO:41. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:41 from nucleotide 1575 to  
10 nucleotide 3038, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:41 from nucleotide 1575 to nucleotide 3038, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:41 from nucleotide 1575 to nucleotide 3038. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the  
15 cDNA sequence of SEQ ID NO:41 from nucleotide 1650 to nucleotide 3038, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:41 from nucleotide 1650 to nucleotide 3038, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:41 from nucleotide 1650 to nucleotide 3038.

20 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:42;
- (b) a fragment of the amino acid sequence of SEQ ID NO:42, the  
25 fragment comprising eight contiguous amino acids of SEQ ID NO:42; and
- (c) the amino acid sequence encoded by the cDNA insert of clone vg3\_1 deposited with the ATCC under accession number PTA-362;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:42. In further preferred  
30 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids

of SEQ ID NO:42, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment comprising the amino acid sequence from amino acid 239 to amino acid 248 of SEQ ID NO:42.

In one embodiment, the present invention provides a composition comprising an  
5 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:43;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:43 from nucleotide 2112, to nucleotide 2363;
- 10 (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vo2\_1 deposited with the ATCC under accession number PTA-362;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vo2\_1 deposited with the ATCC under accession number  
15 PTA-362;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo2\_1 deposited with the ATCC under accession number PTA-362;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA  
20 insert of clone vo2\_1 deposited with the ATCC under accession number PTA-362;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:44;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44 having biological activity, the fragment  
25 comprising eight contiguous amino acids of SEQ ID NO:44;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- 30 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:43.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:43 from nucleotide 2112 to nucleotide 2363; the nucleotide sequence of the full-length protein coding sequence of clone vo2\_1 deposited with the ATCC under accession number PTA-362; or the nucleotide sequence of a mature protein coding sequence of clone vo2\_1 deposited with the ATCC under accession number PTA-362. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vo2\_1 deposited with the ATCC under accession number PTA-362. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:44, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44 having biological activity, the fragment comprising the amino acid sequence from amino acid 37 to amino acid 46 of SEQ ID NO:44.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:43.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:43, but excluding the poly(A) tail at the 3' end of SEQ ID NO:43; and

(ab) the nucleotide sequence of the cDNA insert of clone vo2\_1 deposited with the ATCC under accession number PTA-362;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

5 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:43, but excluding the poly(A) tail at the 3' end of SEQ ID NO:43; and

10 (bb) the nucleotide sequence of the cDNA insert of clone vo2\_1 deposited with the ATCC under accession number PTA-362;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

15 (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:43, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:43 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:43, but  
20 excluding the poly(A) tail at the 3' end of SEQ ID NO:43. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:43 from nucleotide 2112 to nucleotide 2363, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:43 from nucleotide 2112 to nucleotide 2363,  
25 to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:43 from nucleotide 2112 to nucleotide 2363.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

30 (a) the amino acid sequence of SEQ ID NO:44;

(b) a fragment of the amino acid sequence of SEQ ID NO:44, the fragment comprising eight contiguous amino acids of SEQ ID NO:44; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo2\_1 deposited with the ATCC under accession number PTA-362; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:44. In further preferred  
5 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:44, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44 having biological activity, the fragment comprising the amino acid sequence  
10 from amino acid 37 to amino acid 46 of SEQ ID NO:44.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:45;
- 15 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:45 from nucleotide 36 to nucleotide 707;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:45 from nucleotide 393 to nucleotide 707;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vo3\_1 deposited with the ATCC under  
20 accession number PTA-362;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vo3\_1 deposited with the ATCC under accession number PTA-362;
- 25 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo3\_1 deposited with the ATCC under accession number PTA-362;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vo3\_1 deposited with the ATCC under accession number PTA-362;
- 30 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:46;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:46 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:46;

5 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

10 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:45.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:45 from nucleotide 36 to nucleotide 707; the nucleotide sequence of SEQ ID NO:45  
15 from nucleotide 393 to nucleotide 707; the nucleotide sequence of the full-length protein coding sequence of clone vo3\_1 deposited with the ATCC under accession number PTA-362; or the nucleotide sequence of a mature protein coding sequence of clone vo3\_1 deposited with the ATCC under accession number PTA-362. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by  
20 the cDNA insert of clone vo3\_1 deposited with the ATCC under accession number PTA-362. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:46 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:46, or a  
25 polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:46 having biological activity, the fragment comprising the amino acid sequence from amino acid 107 to amino acid 116 of SEQ ID NO:46.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:45.

30 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (aa) SEQ ID NO:45, but excluding the poly(A) tail at the 3' end of SEQ ID NO:45; and

(ab) the nucleotide sequence of the cDNA insert of clone vo3\_1 deposited with the ATCC under accession number PTA-362;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

10 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

15 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:45, but excluding the poly(A) tail at the 3' end of SEQ ID NO:45; and

20 (bb) the nucleotide sequence of the cDNA insert of clone vo3\_1 deposited with the ATCC under accession number PTA-362;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

25 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:45, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:45 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:45, but excluding the poly(A) tail at the 3' end of SEQ ID NO:45. Also preferably the  
30 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:45 from nucleotide 36 to nucleotide 707, and extending contiguously from a nucleotide sequence corresponding to the 5' end



of said sequence of SEQ ID NO:45 from nucleotide 36 to nucleotide 707, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:45 from nucleotide 36 to nucleotide 707. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID  
5 NO:45 from nucleotide 393 to nucleotide 707, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:45 from nucleotide 393 to nucleotide 707, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:45 from nucleotide 393 to nucleotide 707.

In other embodiments, the present invention provides a composition comprising  
10 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:46;
- (b) a fragment of the amino acid sequence of SEQ ID NO:46, the fragment comprising eight contiguous amino acids of SEQ ID NO:46; and
- 15 (c) the amino acid sequence encoded by the cDNA insert of clone vo3\_1 deposited with the ATCC under accession number PTA-362;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:46. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino  
20 acid sequence of SEQ ID NO:46 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:46, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:46 having biological activity, the fragment comprising the amino acid sequence from amino acid 107 to amino acid 116 of SEQ ID NO:46.

25 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:47;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID  
30 NO:47 from nucleotide 74 to nucleotide 295;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:47 from nucleotide 134 to nucleotide 295;

- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vo5\_1 deposited with the ATCC under accession number PTA-362;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vo5\_1 deposited with the ATCC under accession number PTA-362;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo5\_1 deposited with the ATCC under accession number PTA-362;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vo5\_1 deposited with the ATCC under accession number PTA-362;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:48;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:48;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:47.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:47 from nucleotide 74 to nucleotide 295; the nucleotide sequence of SEQ ID NO:47 from nucleotide 134 to nucleotide 295; the nucleotide sequence of the full-length protein coding sequence of clone vo5\_1 deposited with the ATCC under accession number PTA-362; or the nucleotide sequence of a mature protein coding sequence of clone vo5\_1 deposited with the ATCC under accession number PTA-362. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by

the cDNA insert of clone vo5\_1 deposited with the ATCC under accession number PTA-362. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment preferably comprising eight (more preferably  
5 twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:48, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment comprising the amino acid sequence from amino acid 32 to amino acid 41 of SEQ ID NO:48.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ  
10 ID NO:47.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize  
15 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:47, but excluding the poly(A) tail at the 3' end of SEQ ID NO:47; and
    - (ab) the nucleotide sequence of the cDNA insert of clone  
20 vo5\_1 deposited with the ATCC under accession number PTA-362;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
  - (iii) isolating the DNA polynucleotides detected with the probe(s);

25 and

- (b) a process comprising the steps of:
  - (i) preparing one or more polynucleotide primers that hybridize  
in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (ba) SEQ ID NO:47, but excluding the poly(A) tail at the  
30 3' end of SEQ ID NO:47; and

- (bb) the nucleotide sequence of the cDNA insert of clone vo5\_1 deposited with the ATCC under accession number PTA-362;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- 5 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:47, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID

10 NO:47 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:47, but excluding the poly(A) tail at the 3' end of SEQ ID NO:47. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:47 from nucleotide 74 to nucleotide 295, and extending contiguously from a nucleotide sequence corresponding to the 5' end

15 of said sequence of SEQ ID NO:47 from nucleotide 74 to nucleotide 295, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:47 from nucleotide 74 to nucleotide 295. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:47 from nucleotide 134 to nucleotide 295, and extending contiguously from a

20 nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:47 from nucleotide 134 to nucleotide 295, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:47 from nucleotide 134 to nucleotide 295.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group

25 consisting of:

- (a) the amino acid sequence of SEQ ID NO:48;
- (b) a fragment of the amino acid sequence of SEQ ID NO:48, the fragment comprising eight contiguous amino acids of SEQ ID NO:48; and
- (c) the amino acid sequence encoded by the cDNA insert of clone
- 30 vo5\_1 deposited with the ATCC under accession number PTA-362;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:48. In further preferred

embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:48, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment comprising the amino acid sequence from amino acid 32 to amino acid 41 of SEQ ID NO:48.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 10 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:49;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:49 from nucleotide 45 to nucleotide 383;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:49 from nucleotide 312 to nucleotide 383;
- 15 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vo6\_1 deposited with the ATCC under accession number PTA-362;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vo6\_1 deposited with the ATCC under accession number  
20 PTA-362;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo6\_1 deposited with the ATCC under accession number PTA-362;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA  
25 insert of clone vo6\_1 deposited with the ATCC under accession number PTA-362;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:50;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50 having biological activity, the fragment  
30 comprising eight contiguous amino acids of SEQ ID NO:50;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

5 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:49.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:49 from nucleotide 45 to nucleotide 383; the nucleotide sequence of SEQ ID NO:49  
10 from nucleotide 312 to nucleotide 383; the nucleotide sequence of the full-length protein coding sequence of clone vo6\_1 deposited with the ATCC under accession number PTA-362; or the nucleotide sequence of a mature protein coding sequence of clone vo6\_1 deposited with the ATCC under accession number PTA-362. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by  
15 the cDNA insert of clone vo6\_1 deposited with the ATCC under accession number PTA-362. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:50, or a  
20 polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50 having biological activity, the fragment comprising the amino acid sequence from amino acid 51 to amino acid 60 of SEQ ID NO:50.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:49.

25 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the  
30 group consisting of:

(aa) SEQ ID NO:49, but excluding the poly(A) tail at the 3' end of SEQ ID NO:49; and

- (ab) the nucleotide sequence of the cDNA insert of clone vo6\_1 deposited with the ATCC under accession number PTA-362;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 5 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that hybridize
- 10 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:49, but excluding the poly(A) tail at the 3' end of SEQ ID NO:49; and
- (bb) the nucleotide sequence of the cDNA insert of clone
- 15 vo6\_1 deposited with the ATCC under accession number PTA-362;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).
- 20 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:49, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:49 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:49 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:49. Also preferably the
- 25 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:49 from nucleotide 45 to nucleotide 383, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:49 from nucleotide 45 to nucleotide 383, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:49 from nucleotide
- 30 45 to nucleotide 383. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:49 from nucleotide 312 to nucleotide 383, and extending contiguously from a

nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:49 from nucleotide 312 to nucleotide 383, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:49 from nucleotide 312 to nucleotide 383.

In other embodiments, the present invention provides a composition comprising  
5 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:50;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:50, the fragment comprising eight contiguous amino acids of SEQ ID NO:50; and
  - 10 (c) the amino acid sequence encoded by the cDNA insert of clone vo6\_1 deposited with the ATCC under accession number PTA-362;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:50. In further preferred  
15 acid sequence of SEQ ID NO:50 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:50, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50 having biological activity, the fragment comprising the amino acid sequence from amino acid 51 to amino acid 60 of SEQ ID NO:50.

20 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:51;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID  
25 NO:51 from nucleotide 186 to nucleotide 1739;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:51 from nucleotide 288 to nucleotide 1739;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vo9\_1 deposited with the ATCC under  
30 accession number PTA-362;



- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vo9\_1 deposited with the ATCC under accession number PTA-362;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo9\_1 deposited with the ATCC under accession number PTA-362;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vo9\_1 deposited with the ATCC under accession number PTA-362;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:52;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:52;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:51.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:51 from nucleotide 186 to nucleotide 1739; the nucleotide sequence of SEQ ID NO:51 from nucleotide 288 to nucleotide 1739; the nucleotide sequence of the full-length protein coding sequence of clone vo9\_1 deposited with the ATCC under accession number PTA-362; or the nucleotide sequence of a mature protein coding sequence of clone vo9\_1 deposited with the ATCC under accession number PTA-362. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vo9\_1 deposited with the ATCC under accession number PTA-362. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52

having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:52, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52 having biological activity, the fragment comprising the amino acid  
5 sequence from amino acid 254 to amino acid 263 of SEQ ID NO:52.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:51.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 10 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:51, but excluding the poly(A) tail at the  
15 3' end of SEQ ID NO:51; and
    - (ab) the nucleotide sequence of the cDNA insert of clone vo9\_1 deposited with the ATCC under accession number PTA-362;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
  - 20 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that hybridize  
25 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (ba) SEQ ID NO:51, but excluding the poly(A) tail at the 3' end of SEQ ID NO:51; and
    - (bb) the nucleotide sequence of the cDNA insert of clone  
30 vo9\_1 deposited with the ATCC under accession number PTA-362;
  - (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:51, and  
5 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:51 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:51, but excluding the poly(A) tail at the 3' end of SEQ ID NO:51. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:51 from nucleotide 186 to nucleotide  
10 1739, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:51 from nucleotide 186 to nucleotide 1739, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:51 from nucleotide 186 to nucleotide 1739. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID  
15 NO:51 from nucleotide 288 to nucleotide 1739, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:51 from nucleotide 288 to nucleotide 1739, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:51 from nucleotide 288 to nucleotide 1739.

In other embodiments, the present invention provides a composition comprising  
20 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:52;
- (b) a fragment of the amino acid sequence of SEQ ID NO:52, the fragment comprising eight contiguous amino acids of SEQ ID NO:52; and
- 25 (c) the amino acid sequence encoded by the cDNA insert of clone vo9\_1 deposited with the ATCC under accession number PTA-362;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:52. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino  
30 acid sequence of SEQ ID NO:52 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:52, or a protein comprising a fragment of the amino acid sequence of SEQ

ID NO:52 having biological activity, the fragment comprising the amino acid sequence from amino acid 254 to amino acid 263 of SEQ ID NO:52.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 5                   (a)     a polynucleotide comprising the nucleotide sequence of SEQ ID NO:53;
- (b)     a polynucleotide comprising the nucleotide sequence of SEQ ID NO:53 from nucleotide 440 to nucleotide 835;
- (c)     a polynucleotide comprising the nucleotide sequence of SEQ ID  
10               NO:53 from nucleotide 632 to nucleotide 835;
- (d)     a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vo11\_1 deposited with the ATCC under accession number PTA-366;
- (e)     a polynucleotide encoding the full-length protein encoded by the  
15               cDNA insert of clone vo11\_1 deposited with the ATCC under accession number PTA-366;
- (f)     a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo11\_1 deposited with the ATCC under accession number PTA-366;
- 20               (g)     a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vo11\_1 deposited with the ATCC under accession number PTA-366;
- (h)     a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:54;
- 25               (i)     a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:54;
- (j)     a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- 30               (k)     a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:53.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:53 from nucleotide 440 to nucleotide 835; the nucleotide sequence of SEQ ID NO:53 from nucleotide 632 to nucleotide 835; the nucleotide sequence of the full-length protein coding sequence of clone vo11\_1 deposited with the ATCC under accession number PTA-366; or the nucleotide sequence of a mature protein coding sequence of clone vo11\_1 deposited with the ATCC under accession number PTA-366. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vo11\_1 deposited with the ATCC under accession number PTA-366. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:54, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment comprising the amino acid sequence from amino acid 61 to amino acid 70 of SEQ ID NO:54.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:53.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (aa) SEQ ID NO:53, but excluding the poly(A) tail at the 3' end of SEQ ID NO:53; and

- (ab) the nucleotide sequence of the cDNA insert of clone  
vol1\_1 deposited with the ATCC under accession number PTA-366;
- (ii) hybridizing said probe(s) to human genomic DNA in  
conditions at least as stringent as 4X SSC at 50 degrees C; and
- 5 (iii) isolating the DNA polynucleotides detected with the  
probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that hybridize  
10 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the  
group consisting of:
- (ba) SEQ ID NO:53, but excluding the poly(A) tail at the  
3' end of SEQ ID NO:53; and
- (bb) the nucleotide sequence of the cDNA insert of clone  
15 vol1\_1 deposited with the ATCC under accession number PTA-  
366;
- (ii) hybridizing said primer(s) to human genomic DNA in  
conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- 20 (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a  
nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:53, and  
extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID  
NO:53 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:53, but  
25 excluding the poly(A) tail at the 3' end of SEQ ID NO:53. Also preferably the  
polynucleotide isolated according to the above process comprises a nucleotide sequence  
corresponding to the cDNA sequence of SEQ ID NO:53 from nucleotide 440 to nucleotide  
835, and extending contiguously from a nucleotide sequence corresponding to the 5' end  
of said sequence of SEQ ID NO:53 from nucleotide 440 to nucleotide 835, to a nucleotide  
30 sequence corresponding to the 3' end of said sequence of SEQ ID NO:53 from nucleotide  
440 to nucleotide 835. Also preferably the polynucleotide isolated according to the above  
process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID

NO:53 from nucleotide 632 to nucleotide 835, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:53 from nucleotide 632 to nucleotide 835, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:53 from nucleotide 632 to nucleotide 835.

5 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:54;
- (b) a fragment of the amino acid sequence of SEQ ID NO:54, the  
10 fragment comprising eight contiguous amino acids of SEQ ID NO:54; and
- (c) the amino acid sequence encoded by the cDNA insert of clone  
vol11\_1 deposited with the ATCC under accession number PTA-366;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:54. In further preferred  
15 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:54, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment comprising the amino acid sequence  
20 from amino acid 61 to amino acid 70 of SEQ ID NO:54.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID  
NO:55;
- 25 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID  
NO:55 from nucleotide 72 to nucleotide 329;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID  
NO:55 from nucleotide 120 to nucleotide 329;
- (d) a polynucleotide comprising the nucleotide sequence of the full-  
30 length protein coding sequence of clone vol12\_1 deposited with the ATCC under  
accession number PTA-366;

- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vo12\_1 deposited with the ATCC under accession number PTA-366;
- 5 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo12\_1 deposited with the ATCC under accession number PTA-366;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vo12\_1 deposited with the ATCC under accession number PTA-366;
- 10 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:56;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:56;
- 15 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- 20 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:55.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:55 from nucleotide 72 to nucleotide 329; the nucleotide sequence of SEQ ID NO:55 from nucleotide 120 to nucleotide 329; the nucleotide sequence of the full-length protein coding sequence of clone vo12\_1 deposited with the ATCC under accession number PTA-366; or the nucleotide sequence of a mature protein coding sequence of clone vo12\_1 deposited with the ATCC under accession number PTA-366. In other preferred

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30 embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vo12\_1 deposited with the ATCC under accession number PTA-366. In further preferred embodiments, the present invention provides a polynucleotide



encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:56, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of  
5 SEQ ID NO:56 having biological activity, the fragment comprising the amino acid sequence from amino acid 38 to amino acid 47 of SEQ ID NO:56.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:55.

Further embodiments of the invention provide isolated polynucleotides produced  
10 according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

15 (aa) SEQ ID NO:55, but excluding the poly(A) tail at the 3' end of SEQ ID NO:55; and

(ab) the nucleotide sequence of the cDNA insert of clone vo12\_1 deposited with the ATCC under accession number PTA-366;

20 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

25 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

30 (ba) SEQ ID NO:55, but excluding the poly(A) tail at the 3' end of SEQ ID NO:55; and

- (bb) the nucleotide sequence of the cDNA insert of clone vo12\_1 deposited with the ATCC under accession number PTA-366;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- 5 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:55, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID

10 NO:55 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:55, but excluding the poly(A) tail at the 3' end of SEQ ID NO:55. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:55 from nucleotide 72 to nucleotide 329, and extending contiguously from a nucleotide sequence corresponding to the 5' end

15 of said sequence of SEQ ID NO:55 from nucleotide 72 to nucleotide 329, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:55 from nucleotide 72 to nucleotide 329. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:55 from nucleotide 120 to nucleotide 329, and extending contiguously from a

20 nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:55 from nucleotide 120 to nucleotide 329, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:55 from nucleotide 120 to nucleotide 329.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group

25 consisting of:

- (a) the amino acid sequence of SEQ ID NO:56;
- (b) a fragment of the amino acid sequence of SEQ ID NO:56, the fragment comprising eight contiguous amino acids of SEQ ID NO:56; and
- (c) the amino acid sequence encoded by the cDNA insert of clone
- 30 vo12\_1 deposited with the ATCC under accession number PTA-366;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:56. In further preferred

embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:56, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment comprising the amino acid sequence from amino acid 38 to amino acid 47 of SEQ ID NO:56.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 10 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:57;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:57 from nucleotide 227 to nucleotide 439;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:57 from nucleotide 287 to nucleotide 439;
- 15 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vo13\_1 deposited with the ATCC under accession number PTA-366;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vo13\_1 deposited with the ATCC under accession number PTA-366;
- 20 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo13\_1 deposited with the ATCC under accession number PTA-366;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vo13\_1 deposited with the ATCC under accession number PTA-366;
- 25 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:58;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:58;
- 30

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

5 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:57.

10 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:57 from nucleotide 227 to nucleotide 439; the nucleotide sequence of SEQ ID NO:57 from nucleotide 287 to nucleotide 439; the nucleotide sequence of the full-length protein coding sequence of clone vo13\_1 deposited with the ATCC under accession number PTA-366; or the nucleotide sequence of a mature protein coding sequence of clone vo13\_1  
15 deposited with the ATCC under accession number PTA-366. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vo13\_1 deposited with the ATCC under accession number PTA-366. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58  
20 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:58, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58 having biological activity, the fragment comprising the amino acid sequence from amino acid 30 to amino acid 39 of SEQ ID NO:58.

25 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:57.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

30 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- (aa) SEQ ID NO:57, but excluding the poly(A) tail at the 3' end of SEQ ID NO:57; and
- (ab) the nucleotide sequence of the cDNA insert of clone vo13\_1 deposited with the ATCC under accession number PTA-366;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:57, but excluding the poly(A) tail at the 3' end of SEQ ID NO:57; and
- (bb) the nucleotide sequence of the cDNA insert of clone vo13\_1 deposited with the ATCC under accession number PTA-366;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:57, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:57 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:57, but excluding the poly(A) tail at the 3' end of SEQ ID NO:57. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:57 from nucleotide 227 to nucleotide 439, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:57 from nucleotide 227 to nucleotide 439, to a nucleotide

sequence corresponding to the 3' end of said sequence of SEQ ID NO:57 from nucleotide 227 to nucleotide 439. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:57 from nucleotide 287 to nucleotide 439, and extending contiguously from a  
5 nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:57 from nucleotide 287 to nucleotide 439, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:57 from nucleotide 287 to nucleotide 439.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group  
10 consisting of:

- (a) the amino acid sequence of SEQ ID NO:58;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:58, the fragment comprising eight contiguous amino acids of SEQ ID NO:58; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone  
15 vo13\_1 deposited with the ATCC under accession number PTA-366;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:58. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58 having biological activity, the fragment preferably  
20 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:58, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58 having biological activity, the fragment comprising the amino acid sequence from amino acid 30 to amino acid 39 of SEQ ID NO:58.

In one embodiment, the present invention provides a composition comprising an  
25 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:59;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:59 from nucleotide 96 to nucleotide 341;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID  
30 NO:59 from nucleotide 174 to nucleotide 341;

- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vo14\_1 deposited with the ATCC under accession number PTA-366;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vo14\_1 deposited with the ATCC under accession number PTA-366;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo14\_1 deposited with the ATCC under accession number PTA-366;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vo14\_1 deposited with the ATCC under accession number PTA-366;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:60;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:60;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:59.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:59 from nucleotide 96 to nucleotide 341; the nucleotide sequence of SEQ ID NO:59 from nucleotide 174 to nucleotide 341; the nucleotide sequence of the full-length protein coding sequence of clone vo14\_1 deposited with the ATCC under accession number PTA-366; or the nucleotide sequence of a mature protein coding sequence of clone vo14\_1 deposited with the ATCC under accession number PTA-366. In other preferred

embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vo14\_1 deposited with the ATCC under accession number PTA-366. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60  
5 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:60, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60 having biological activity, the fragment comprising the amino acid sequence from amino acid 36 to amino acid 45 of SEQ ID NO:60.

10 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:59.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - 15 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:59, but excluding the poly(A) tail at the 3' end of SEQ ID NO:59; and
    - 20 (ab) the nucleotide sequence of the cDNA insert of clone vo14\_1 deposited with the ATCC under accession number PTA-366;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
  - 25 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:
  - (i) preparing one or more polynucleotide primers that hybridize  
30 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:



- (ba) SEQ ID NO:59, but excluding the poly(A) tail at the 3' end of SEQ ID NO:59; and
- (bb) the nucleotide sequence of the cDNA insert of clone vol4\_1 deposited with the ATCC under accession number PTA-366;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).
- 10 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:59, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:59 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:59, but excluding the poly(A) tail at the 3' end of SEQ ID NO:59. Also preferably the
- 15 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:59 from nucleotide 96 to nucleotide 341, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:59 from nucleotide 96 to nucleotide 341, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:59 from nucleotide
- 20 96 to nucleotide 341. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:59 from nucleotide 174 to nucleotide 341, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:59 from nucleotide 174 to nucleotide 341, to a nucleotide sequence corresponding to the 3' end of
- 25 said sequence of SEQ ID NO:59 from nucleotide 174 to nucleotide 341.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:60;
- 30 (b) a fragment of the amino acid sequence of SEQ ID NO:60, the fragment comprising eight contiguous amino acids of SEQ ID NO:60; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo14\_1 deposited with the ATCC under accession number PTA-366; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:60. In further preferred  
5 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:60, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60 having biological activity, the fragment comprising the amino acid sequence  
10 from amino acid 36 to amino acid 45 of SEQ ID NO:60.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:61;
- 15 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:61 from nucleotide 90 to nucleotide 599;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:61 from nucleotide 165 to nucleotide 599;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vo15\_1 deposited with the ATCC under  
20 accession number PTA-366;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vo15\_1 deposited with the ATCC under accession number PTA-366;
- 25 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo15\_1 deposited with the ATCC under accession number PTA-366;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vo15\_1 deposited with the ATCC under accession number PTA-  
30 366;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:62;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:62;

5 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

10 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:61.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:61 from nucleotide 90 to nucleotide 599; the nucleotide sequence of SEQ ID NO:61 from nucleotide 165 to nucleotide 599; the nucleotide sequence of the full-length protein coding sequence of clone vo15\_1 deposited with the ATCC under accession number PTA-366; or the nucleotide sequence of a mature protein coding sequence of clone vo15\_1 deposited with the ATCC under accession number PTA-366. In other preferred  
15 embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vo15\_1 deposited with the ATCC under accession number PTA-366. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:62, or a  
20 polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62 having biological activity, the fragment comprising the amino acid sequence from amino acid 80 to amino acid 89 of SEQ ID NO:62.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:61.

30 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (aa) SEQ ID NO:61, but excluding the poly(A) tail at the 3' end of SEQ ID NO:61; and

(ab) the nucleotide sequence of the cDNA insert of clone vo15\_1 deposited with the ATCC under accession number PTA-366;

10 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

15 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:61, but excluding the poly(A) tail at the 3' end of SEQ ID NO:61; and

20 (bb) the nucleotide sequence of the cDNA insert of clone vo15\_1 deposited with the ATCC under accession number PTA-366;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

25 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:61, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID  
30 NO:61 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:61, but excluding the poly(A) tail at the 3' end of SEQ ID NO:61. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence

corresponding to the cDNA sequence of SEQ ID NO:61 from nucleotide 90 to nucleotide 599, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:61 from nucleotide 90 to nucleotide 599, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:61 from nucleotide 90 to nucleotide 599. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:61 from nucleotide 165 to nucleotide 599, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:61 from nucleotide 165 to nucleotide 599, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:61 from nucleotide 165 to nucleotide 599.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:62;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:62, the fragment comprising eight contiguous amino acids of SEQ ID NO:62; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone vo15\_1 deposited with the ATCC under accession number PTA-366;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:62. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:62, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62 having biological activity, the fragment comprising the amino acid sequence from amino acid 80 to amino acid 89 of SEQ ID NO:62.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:63;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:63 from nucleotide 209 to nucleotide 451;

- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:63 from nucleotide 398 to nucleotide 451;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vo16\_1 deposited with the ATCC under accession number PTA-366;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vo16\_1 deposited with the ATCC under accession number PTA-366;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo16\_1 deposited with the ATCC under accession number PTA-366;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vo16\_1 deposited with the ATCC under accession number PTA-366;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:64;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:64;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:63.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:63 from nucleotide 209 to nucleotide 451; the nucleotide sequence of SEQ ID NO:63 from nucleotide 398 to nucleotide 451; the nucleotide sequence of the full-length protein coding sequence of clone vo16\_1 deposited with the ATCC under accession number PTA-

366; or the nucleotide sequence of a mature protein coding sequence of clone vo16\_1 deposited with the ATCC under accession number PTA-366. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vo16\_1 deposited with the ATCC under accession number PTA-  
5 366. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:64, or a  
10 polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64 having biological activity, the fragment comprising the amino acid sequence from amino acid 35 to amino acid 44 of SEQ ID NO:64.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:63.

Further embodiments of the invention provide isolated polynucleotides produced  
15 according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

20 (aa) SEQ ID NO:63, but excluding the poly(A) tail at the 3' end of SEQ ID NO:63; and

(ab) the nucleotide sequence of the cDNA insert of clone vo16\_1 deposited with the ATCC under accession number PTA-366;

25 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

30 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (ba) SEQ ID NO:63, but excluding the poly(A) tail at the 3' end of SEQ ID NO:63; and

(bb) the nucleotide sequence of the cDNA insert of clone vo16\_1 deposited with the ATCC under accession number PTA-366;

10 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:63, and  
15 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:63 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:63, but excluding the poly(A) tail at the 3' end of SEQ ID NO:63. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:63 from nucleotide  
20 451, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:63 from nucleotide 209 to nucleotide 451, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:63 from nucleotide 209 to nucleotide 451. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID  
25 NO:63 from nucleotide 398 to nucleotide 451, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:63 from nucleotide 398 to nucleotide 451, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:63 from nucleotide 398 to nucleotide 451.

In other embodiments, the present invention provides a composition comprising  
30 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:64;



- (b) a fragment of the amino acid sequence of SEQ ID NO:64, the fragment comprising eight contiguous amino acids of SEQ ID NO:64; and
- (c) the amino acid sequence encoded by the cDNA insert of clone vo16\_1 deposited with the ATCC under accession number PTA-366;
- 5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:64. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 10 of SEQ ID NO:64, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64 having biological activity, the fragment comprising the amino acid sequence from amino acid 35 to amino acid 44 of SEQ ID NO:64.

In one embodiment, the present invention provides a composition comprising an

15 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:65;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:65 from nucleotide 31 to nucleotide 231;
- 20 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:65 from nucleotide 97 to nucleotide 231;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vo18\_1 deposited with the ATCC under accession number PTA-366;
- 25 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vo18\_1 deposited with the ATCC under accession number PTA-366;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo18\_1 deposited with the ATCC under
- 30 accession number PTA-366;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vo18\_1 deposited with the ATCC under accession number PTA-366;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:66;

5 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:66 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:66;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

10 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

15 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:65.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:65 from nucleotide 31 to nucleotide 231; the nucleotide sequence of SEQ ID NO:65 from nucleotide 97 to nucleotide 231; the nucleotide sequence of the full-length protein coding sequence of clone vo18\_1 deposited with the ATCC under accession number PTA-  
20 366; or the nucleotide sequence of a mature protein coding sequence of clone vo18\_1 deposited with the ATCC under accession number PTA-366. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vo18\_1 deposited with the ATCC under accession number PTA-  
25 366. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:66 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:66, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of  
30 SEQ ID NO:66 having biological activity, the fragment comprising the amino acid sequence from amino acid 28 to amino acid 37 of SEQ ID NO:66.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:65.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 5 (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - 10 (aa) SEQ ID NO:65, but excluding the poly(A) tail at the 3' end of SEQ ID NO:65; and
    - (ab) the nucleotide sequence of the cDNA insert of clone vo18\_1 deposited with the ATCC under accession number PTA-366;
  - (ii) hybridizing said probe(s) to human genomic DNA in  
15 conditions at least as stringent as 4X SSC at 50 degrees C; and
  - (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
  - 20 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (ba) SEQ ID NO:65, but excluding the poly(A) tail at the 3' end of SEQ ID NO:65; and
    - 25 (bb) the nucleotide sequence of the cDNA insert of clone vo18\_1 deposited with the ATCC under accession number PTA-366;
  - (ii) hybridizing said primer(s) to human genomic DNA in  
conditions at least as stringent as 4X SSC at 50 degrees C;
  - 30 (iii) amplifying human DNA sequences; and
  - (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:65, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:65 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:65, but  
5 excluding the poly(A) tail at the 3' end of SEQ ID NO:65. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:65 from nucleotide 31 to nucleotide 231, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:65 from nucleotide 31 to nucleotide 231, to a nucleotide  
10 sequence corresponding to the 3' end of said sequence of SEQ ID NO:65 from nucleotide 31 to nucleotide 231. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:65 from nucleotide 97 to nucleotide 231, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:65 from  
15 nucleotide 97 to nucleotide 231, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:65 from nucleotide 97 to nucleotide 231.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 20 (a) the amino acid sequence of SEQ ID NO:66;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:66, the fragment comprising eight contiguous amino acids of SEQ ID NO:66; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone vo18\_1 deposited with the ATCC under accession number PTA-366;
- 25 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:66. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:66 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids  
30 of SEQ ID NO:66, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:66 having biological activity, the fragment comprising the amino acid sequence from amino acid 28 to amino acid 37 of SEQ ID NO:66.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:67;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:67 from nucleotide 23 to nucleotide 736;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:67 from nucleotide 83 to nucleotide 736;
- 10 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vo19\_1 deposited with the ATCC under accession number PTA-366;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vo19\_1 deposited with the ATCC under accession number PTA-366;
- 15 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo19\_1 deposited with the ATCC under accession number PTA-366;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vo19\_1 deposited with the ATCC under accession number PTA-366;
- 20 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:68;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:68 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:68;
- 25 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 30 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:67.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:67 from nucleotide 23 to nucleotide 736; the nucleotide sequence of SEQ ID NO:67 from nucleotide 83 to nucleotide 736; the nucleotide sequence of the full-length protein coding sequence of clone vo19\_1 deposited with the ATCC under accession number PTA-366; or the nucleotide sequence of a mature protein coding sequence of clone vo19\_1 deposited with the ATCC under accession number PTA-366. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vo19\_1 deposited with the ATCC under accession number PTA-366. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:68 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:68, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:68 having biological activity, the fragment comprising the amino acid sequence from amino acid 114 to amino acid 123 of SEQ ID NO:68.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:67.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:67, but excluding the poly(A) tail at the 3' end of SEQ ID NO:67; and
    - (ab) the nucleotide sequence of the cDNA insert of clone vo19\_1 deposited with the ATCC under accession number PTA-366;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

5 and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

10 (ba) SEQ ID NO:67, but excluding the poly(A) tail at the 3' end of SEQ ID NO:67; and

(bb) the nucleotide sequence of the cDNA insert of clone vo19\_1 deposited with the ATCC under accession number PTA-366;

15 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a  
20 nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:67, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:67 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:67, but excluding the poly(A) tail at the 3' end of SEQ ID NO:67. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence  
25 corresponding to the cDNA sequence of SEQ ID NO:67 from nucleotide 23 to nucleotide 736, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:67 from nucleotide 23 to nucleotide 736, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:67 from nucleotide 23 to nucleotide 736. Also preferably the polynucleotide isolated according to the above  
30 process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:67 from nucleotide 83 to nucleotide 736, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:67 from

nucleotide 83 to nucleotide 736, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:67 from nucleotide 83 to nucleotide 736.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group  
5 consisting of:

- (a) the amino acid sequence of SEQ ID NO:68;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:68, the fragment comprising eight contiguous amino acids of SEQ ID NO:68; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone  
10 vo19\_1 deposited with the ATCC under accession number PTA-366;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:68. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:68 having biological activity, the fragment preferably  
15 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:68, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:68 having biological activity, the fragment comprising the amino acid sequence from amino acid 114 to amino acid 123 of SEQ ID NO:68.

In one embodiment, the present invention provides a composition comprising an  
20 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:69;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:69 from nucleotide 104 to nucleotide 1399;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID  
25 NO:69 from nucleotide 158 to nucleotide 1399;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vo22\_1 deposited with the ATCC under accession number PTA-366;
- (e) a polynucleotide encoding the full-length protein encoded by the  
30 cDNA insert of clone vo22\_1 deposited with the ATCC under accession number PTA-366;



(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo22\_1 deposited with the ATCC under accession number PTA-366;

5 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vo22\_1 deposited with the ATCC under accession number PTA-366;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:70;

10 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:70 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:70;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

15 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

20 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:69.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:69 from nucleotide 104 to nucleotide 1399; the nucleotide sequence of SEQ ID NO:69 from nucleotide 158 to nucleotide 1399; the nucleotide sequence of the full-length protein coding sequence of clone vo22\_1 deposited with the ATCC under accession number PTA-366; or the nucleotide sequence of a mature protein coding sequence of clone vo22\_1 deposited with the ATCC under accession number PTA-366. In other preferred  
25 embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vo22\_1 deposited with the ATCC under accession number PTA-366. In further preferred embodiments, the present invention provides a polynucleotide  
30 encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:70 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:70, or a

polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:70 having biological activity, the fragment comprising the amino acid sequence from amino acid 211 to amino acid 220 of SEQ ID NO:70.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:69.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
    - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
      - (aa) SEQ ID NO:69, but excluding the poly(A) tail at the 3' end of SEQ ID NO:69; and
      - (ab) the nucleotide sequence of the cDNA insert of clone vo22\_1 deposited with the ATCC under accession number PTA-366;
    - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
    - (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
    - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
      - (ba) SEQ ID NO:69, but excluding the poly(A) tail at the 3' end of SEQ ID NO:69; and
      - (bb) the nucleotide sequence of the cDNA insert of clone vo22\_1 deposited with the ATCC under accession number PTA-366;
    - (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:69, and  
5 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:69 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:69, but excluding the poly(A) tail at the 3' end of SEQ ID NO:69. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:69 from nucleotide 104 to nucleotide  
10 1399, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:69 from nucleotide 104 to nucleotide 1399, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:69 from nucleotide 104 to nucleotide 1399. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID  
15 NO:69 from nucleotide 158 to nucleotide 1399, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:69 from nucleotide 158 to nucleotide 1399, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:69 from nucleotide 158 to nucleotide 1399.

In other embodiments, the present invention provides a composition comprising  
20 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:70;
- (b) a fragment of the amino acid sequence of SEQ ID NO:70, the fragment comprising eight contiguous amino acids of SEQ ID NO:70; and
- 25 (c) the amino acid sequence encoded by the cDNA insert of clone vo22\_1 deposited with the ATCC under accession number PTA-366;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:70. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino  
30 acid sequence of SEQ ID NO:70 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:70, or a protein comprising a fragment of the amino acid sequence of SEQ

ID NO:70 having biological activity, the fragment comprising the amino acid sequence from amino acid 211 to amino acid 220 of SEQ ID NO:70.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 5                   (a)     a polynucleotide comprising the nucleotide sequence of SEQ ID NO:71;
- (b)     a polynucleotide comprising the nucleotide sequence of SEQ ID NO:71 from nucleotide 174 to nucleotide 1595;
- (c)     a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vo23\_1 deposited with the ATCC under  
10                   accession number PTA-366;
- (d)     a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vo23\_1 deposited with the ATCC under accession number PTA-366;
- 15                   (e)     a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo23\_1 deposited with the ATCC under accession number PTA-366;
- (f)     a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vo23\_1 deposited with the ATCC under accession number PTA-  
20                   366;
- (g)     a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:72;
- (h)     a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:72 having biological activity, the fragment  
25                   comprising eight contiguous amino acids of SEQ ID NO:72;
- (i)     a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j)     a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- 30                   (k)     a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:71.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:71 from nucleotide 174 to nucleotide 1595; the nucleotide sequence of the full-length protein coding sequence of clone vo23\_1 deposited with the ATCC under accession number PTA-366; or the nucleotide sequence of a mature protein coding sequence of clone vo23\_1 deposited with the ATCC under accession number PTA-366. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vo23\_1 deposited with the ATCC under accession number PTA-366. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:72 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:72, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:72 having biological activity, the fragment comprising the amino acid sequence from amino acid 232 to amino acid 241 of SEQ ID NO:72.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:71.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:71, but excluding the poly(A) tail at the 3' end of SEQ ID NO:71; and

(ab) the nucleotide sequence of the cDNA insert of clone vo23\_1 deposited with the ATCC under accession number PTA-366;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

5 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:71, but excluding the poly(A) tail at the 3' end of SEQ ID NO:71; and

10 (bb) the nucleotide sequence of the cDNA insert of clone vo23\_1 deposited with the ATCC under accession number PTA-366;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

15 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:71, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:71 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:71, but  
20 excluding the poly(A) tail at the 3' end of SEQ ID NO:71. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:71 from nucleotide 174 to nucleotide 1595, and extending contiguously from a nucleotide sequence corresponding to the 5' end  
25 of said sequence of SEQ ID NO:71 from nucleotide 174 to nucleotide 1595, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:71 from nucleotide 174 to nucleotide 1595.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group  
30 consisting of:

(a) the amino acid sequence of SEQ ID NO:72;

(b) a fragment of the amino acid sequence of SEQ ID NO:72, the fragment comprising eight contiguous amino acids of SEQ ID NO:72; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo23\_1 deposited with the ATCC under accession number PTA-366;

5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:72. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:72 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids  
10 of SEQ ID NO:72, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:72 having biological activity, the fragment comprising the amino acid sequence from amino acid 232 to amino acid 241 of SEQ ID NO:72.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

15 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:73;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:73 from nucleotide 129 to nucleotide 311;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID  
20 NO:73 from nucleotide 195 to nucleotide 311;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vo24\_1 deposited with the ATCC under accession number PTA-366;

(e) a polynucleotide encoding the full-length protein encoded by the  
25 cDNA insert of clone vo24\_1 deposited with the ATCC under accession number PTA-366;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo24\_1 deposited with the ATCC under accession number PTA-366;

30 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vo24\_1 deposited with the ATCC under accession number PTA-366;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:74;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:74 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:74;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:73.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:73 from nucleotide 129 to nucleotide 311; the nucleotide sequence of SEQ ID NO:73 from nucleotide 195 to nucleotide 311; the nucleotide sequence of the full-length protein coding sequence of clone vo24\_1 deposited with the ATCC under accession number PTA-366; or the nucleotide sequence of a mature protein coding sequence of clone vo24\_1 deposited with the ATCC under accession number PTA-366. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vo24\_1 deposited with the ATCC under accession number PTA-366. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:74 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:74, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:74 having biological activity, the fragment comprising the amino acid sequence from amino acid 25 to amino acid 34 of SEQ ID NO:74.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:73.



Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:73, but excluding the poly(A) tail at the 3' end of SEQ ID NO:73; and

(ab) the nucleotide sequence of the cDNA insert of clone vo24\_1 deposited with the ATCC under accession number PTA-366;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:73, but excluding the poly(A) tail at the 3' end of SEQ ID NO:73; and

(bb) the nucleotide sequence of the cDNA insert of clone vo24\_1 deposited with the ATCC under accession number PTA-366;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:73, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID

NO:73 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:73 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:73. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:73 from nucleotide 129 to nucleotide 311, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:73 from nucleotide 129 to nucleotide 311, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:73 from nucleotide 129 to nucleotide 311. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:73 from nucleotide 195 to nucleotide 311, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:73 from nucleotide 195 to nucleotide 311, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:73 from nucleotide 195 to nucleotide 311.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:74;
- (b) a fragment of the amino acid sequence of SEQ ID NO:74, the fragment comprising eight contiguous amino acids of SEQ ID NO:74; and
- (c) the amino acid sequence encoded by the cDNA insert of clone vo24\_1 deposited with the ATCC under accession number PTA-366;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:74. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:74 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:74, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:74 having biological activity, the fragment comprising the amino acid sequence from amino acid 25 to amino acid 34 of SEQ ID NO:74.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:75;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:75 from nucleotide 73 to nucleotide 798;
- 5 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:75 from nucleotide 142 to nucleotide 798;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vo25\_1 deposited with the ATCC under accession number PTA-366;
- 10 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vo25\_1 deposited with the ATCC under accession number PTA-366;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo25\_1 deposited with the ATCC under accession number PTA-366;
- 15 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vo25\_1 deposited with the ATCC under accession number PTA-366;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:76;
- 20 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:76;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- 25 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- 30 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:75.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:75 from nucleotide 73 to nucleotide 798; the nucleotide sequence of SEQ ID NO:75 from nucleotide 142 to nucleotide 798; the nucleotide sequence of the full-length protein coding sequence of clone vo25\_1 deposited with the ATCC under accession number PTA-366; or the nucleotide sequence of a mature protein coding sequence of clone vo25\_1 deposited with the ATCC under accession number PTA-366. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vo25\_1 deposited with the ATCC under accession number PTA-366. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:76, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76 having biological activity, the fragment comprising the amino acid sequence from amino acid 116 to amino acid 125 of SEQ ID NO:76.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:75.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:75, but excluding the poly(A) tail at the 3' end of SEQ ID NO:75; and
    - (ab) the nucleotide sequence of the cDNA insert of clone vo25\_1 deposited with the ATCC under accession number PTA-366;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
  - (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:75, but excluding the poly(A) tail at the 3' end of SEQ ID NO:75; and

(bb) the nucleotide sequence of the cDNA insert of clone vo25\_1 deposited with the ATCC under accession number PTA-366;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

15 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:75, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:75 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:75, but excluding the poly(A) tail at the 3' end of SEQ ID NO:75. Also preferably the  
20 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:75 from nucleotide 73 to nucleotide 798, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:75 from nucleotide 73 to nucleotide 798, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:75 from nucleotide  
25 73 to nucleotide 798. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:75 from nucleotide 142 to nucleotide 798, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:75 from nucleotide 142 to nucleotide 798, to a nucleotide sequence corresponding to the 3' end of  
30 said sequence of SEQ ID NO:75 from nucleotide 142 to nucleotide 798.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:76;
- 5 (b) a fragment of the amino acid sequence of SEQ ID NO:76, the fragment comprising eight contiguous amino acids of SEQ ID NO:76; and
- (c) the amino acid sequence encoded by the cDNA insert of clone vo25\_1 deposited with the ATCC under accession number PTA-366;

the protein being substantially free from other mammalian proteins. Preferably such  
10 protein comprises the amino acid sequence of SEQ ID NO:76. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:76, or a protein comprising a fragment of the amino acid sequence of SEQ  
15 ID NO:76 having biological activity, the fragment comprising the amino acid sequence from amino acid 116 to amino acid 125 of SEQ ID NO:76.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID  
20 NO:77;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:77 from nucleotide 26 to nucleotide 307;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:77 from nucleotide 101 to nucleotide 307;
- 25 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vo26\_1 deposited with the ATCC under accession number PTA-366;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vo26\_1 deposited with the ATCC under accession number  
30 PTA-366;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo26\_1 deposited with the ATCC under accession number PTA-366;

5 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vo26\_1 deposited with the ATCC under accession number PTA-366;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:78;

10 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:78 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:78;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

15 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

20 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:77.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:77 from nucleotide 26 to nucleotide 307; the nucleotide sequence of SEQ ID NO:77 from nucleotide 101 to nucleotide 307; the nucleotide sequence of the full-length protein coding sequence of clone vo26\_1 deposited with the ATCC under accession number PTA-366; or the nucleotide sequence of a mature protein coding sequence of clone vo26\_1 deposited with the ATCC under accession number PTA-366. In other preferred  
25 embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vo26\_1 deposited with the ATCC under accession number PTA-366. In further preferred embodiments, the present invention provides a polynucleotide  
30 encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:78 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:78, or a

polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:78 having biological activity, the fragment comprising the amino acid sequence from amino acid 42 to amino acid 51 of SEQ ID NO:78.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:77.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
    - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
      - (aa) SEQ ID NO:77, but excluding the poly(A) tail at the 3' end of SEQ ID NO:77; and
      - (ab) the nucleotide sequence of the cDNA insert of clone vo26\_1 deposited with the ATCC under accession number PTA-366;
    - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
    - (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
    - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
      - (ba) SEQ ID NO:77, but excluding the poly(A) tail at the 3' end of SEQ ID NO:77; and
      - (bb) the nucleotide sequence of the cDNA insert of clone vo26\_1 deposited with the ATCC under accession number PTA-366;
    - (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;



- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:77, and  
5 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:77 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:77, but excluding the poly(A) tail at the 3' end of SEQ ID NO:77. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:77 from nucleotide 26 to nucleotide  
10 307, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:77 from nucleotide 26 to nucleotide 307, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:77 from nucleotide 26 to nucleotide 307. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID  
15 NO:77 from nucleotide 101 to nucleotide 307, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:77 from nucleotide 101 to nucleotide 307, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:77 from nucleotide 101 to nucleotide 307.

In other embodiments, the present invention provides a composition comprising  
20 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:78;
- (b) a fragment of the amino acid sequence of SEQ ID NO:78, the fragment comprising eight contiguous amino acids of SEQ ID NO:78; and
- 25 (c) the amino acid sequence encoded by the cDNA insert of clone vo26\_1 deposited with the ATCC under accession number PTA-366;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:78. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino  
30 acid sequence of SEQ ID NO:78 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:78, or a protein comprising a fragment of the amino acid sequence of SEQ

ID NO:78 having biological activity, the fragment comprising the amino acid sequence from amino acid 42 to amino acid 51 of SEQ ID NO:78.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 5                   (a)     a polynucleotide comprising the nucleotide sequence of SEQ ID NO:79;
- (b)     a polynucleotide comprising the nucleotide sequence of SEQ ID NO:79 from nucleotide 43 to nucleotide 228;
- (c)     a polynucleotide comprising the nucleotide sequence of SEQ ID  
10               NO:79 from nucleotide 94 to nucleotide 228;
- (d)     a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vp23\_1 deposited with the ATCC under accession number PTA-368;
- (e)     a polynucleotide encoding the full-length protein encoded by the  
15               cDNA insert of clone vp23\_1 deposited with the ATCC under accession number PTA-368;
- (f)     a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vp23\_1 deposited with the ATCC under accession number PTA-368;
- 20               (g)     a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vp23\_1 deposited with the ATCC under accession number PTA-368;
- (h)     a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:80;
- 25               (i)     a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:80;
- (j)     a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- 30               (k)     a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:79.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:79 from nucleotide 43 to nucleotide 228; the nucleotide sequence of SEQ ID NO:79 from nucleotide 94 to nucleotide 228; the nucleotide sequence of the full-length protein coding sequence of clone vp23\_1 deposited with the ATCC under accession number PTA-368; or the nucleotide sequence of a mature protein coding sequence of clone vp23\_1 deposited with the ATCC under accession number PTA-368. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vp23\_1 deposited with the ATCC under accession number PTA-368. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:80, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the fragment comprising the amino acid sequence from amino acid 26 to amino acid 35 of SEQ ID NO:80.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:79.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:79, but excluding the poly(A) tail at the 3' end of SEQ ID NO:79; and

- (ab) the nucleotide sequence of the cDNA insert of clone  
vp23\_1 deposited with the ATCC under accession number PTA-368;
- (ii) hybridizing said probe(s) to human genomic DNA in  
conditions at least as stringent as 4X SSC at 50 degrees C; and
- 5 (iii) isolating the DNA polynucleotides detected with the  
probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that hybridize  
10 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the  
group consisting of:
- (ba) SEQ ID NO:79, but excluding the poly(A) tail at the  
3' end of SEQ ID NO:79; and
- (bb) the nucleotide sequence of the cDNA insert of clone  
15 vp23\_1 deposited with the ATCC under accession number PTA-  
368;
- (ii) hybridizing said primer(s) to human genomic DNA in  
conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- 20 (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a  
nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:79, and  
extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID  
NO:79 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:79 , but  
25 excluding the poly(A) tail at the 3' end of SEQ ID NO:79. Also preferably the  
polynucleotide isolated according to the above process comprises a nucleotide sequence  
corresponding to the cDNA sequence of SEQ ID NO:79 from nucleotide 43 to nucleotide  
228, and extending contiguously from a nucleotide sequence corresponding to the 5' end  
of said sequence of SEQ ID NO:79 from nucleotide 43 to nucleotide 228, to a nucleotide  
30 sequence corresponding to the 3' end of said sequence of SEQ ID NO:79 from nucleotide  
43 to nucleotide 228. Also preferably the polynucleotide isolated according to the above  
process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID

NO:79 from nucleotide 94 to nucleotide 228, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:79 from nucleotide 94 to nucleotide 228, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:79 from nucleotide 94 to nucleotide 228.

5 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:80;
- (b) a fragment of the amino acid sequence of SEQ ID NO:80, the  
10 fragment comprising eight contiguous amino acids of SEQ ID NO:80; and
- (c) the amino acid sequence encoded by the cDNA insert of clone  
vp23\_1 deposited with the ATCC under accession number PTA-368;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:80. In further preferred  
15 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:80, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the fragment comprising the amino acid sequence  
20 from amino acid 26 to amino acid 35 of SEQ ID NO:80.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID  
NO:81;
- 25 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID  
NO:81 from nucleotide 245 to nucleotide 427;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID  
NO:81 from nucleotide 308 to nucleotide 427;
- (d) a polynucleotide comprising the nucleotide sequence of the full-  
30 length protein coding sequence of clone vq7\_1 deposited with the ATCC under  
accession number PTA-368;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vq7\_1 deposited with the ATCC under accession number PTA-368;

5 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vq7\_1 deposited with the ATCC under accession number PTA-368;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vq7\_1 deposited with the ATCC under accession number PTA-368;

10 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:82;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:82 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:82;

15 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

20 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:81.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:81 from nucleotide 245 to nucleotide 427; the nucleotide sequence of SEQ ID NO:81  
25 from nucleotide 308 to nucleotide 427; the nucleotide sequence of the full-length protein coding sequence of clone vq7\_1 deposited with the ATCC under accession number PTA-368; or the nucleotide sequence of a mature protein coding sequence of clone vq7\_1 deposited with the ATCC under accession number PTA-368. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by  
30 the cDNA insert of clone vq7\_1 deposited with the ATCC under accession number PTA-368. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:82

having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:82, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:82 having biological activity, the fragment comprising the amino acid  
5 sequence from amino acid 25 to amino acid 34 of SEQ ID NO:82.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:81.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 10 (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:81, but excluding the poly(A) tail at the  
15 3' end of SEQ ID NO:81; and
    - (ab) the nucleotide sequence of the cDNA insert of clone vq7\_1 deposited with the ATCC under accession number PTA-368;
    - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
    - 20 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
  - (i) preparing one or more polynucleotide primers that hybridize  
25 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (ba) SEQ ID NO:81, but excluding the poly(A) tail at the 3' end of SEQ ID NO:81; and
    - (bb) the nucleotide sequence of the cDNA insert of clone vq7\_1 deposited with the ATCC under accession number PTA-368;
    - 30 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:81, and  
5 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:81 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:81, but excluding the poly(A) tail at the 3' end of SEQ ID NO:81. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:81 from nucleotide 245 to nucleotide  
10 427, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:81 from nucleotide 245 to nucleotide 427, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:81 from nucleotide 245 to nucleotide 427. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID  
15 NO:81 from nucleotide 308 to nucleotide 427, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:81 from nucleotide 308 to nucleotide 427, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:81 from nucleotide 308 to nucleotide 427.

In other embodiments, the present invention provides a composition comprising  
20 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:82;
- (b) a fragment of the amino acid sequence of SEQ ID NO:82, the fragment comprising eight contiguous amino acids of SEQ ID NO:82; and
- 25 (c) the amino acid sequence encoded by the cDNA insert of clone vq7\_1 deposited with the ATCC under accession number PTA-368;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:82. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino  
30 acid sequence of SEQ ID NO:82 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:82, or a protein comprising a fragment of the amino acid sequence of SEQ



ID NO:82 having biological activity, the fragment comprising the amino acid sequence from amino acid 25 to amino acid 34 of SEQ ID NO:82.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 5                   (a)     a polynucleotide comprising the nucleotide sequence of SEQ ID NO:83;
- (b)     a polynucleotide comprising the nucleotide sequence of SEQ ID NO:83 from nucleotide 119 to nucleotide 475;
- (c)     a polynucleotide comprising the nucleotide sequence of SEQ ID  
10               NO:83 from nucleotide 185 to nucleotide 475;
- (d)     a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vq8\_1 deposited with the ATCC under accession number PTA-368;
- (e)     a polynucleotide encoding the full-length protein encoded by the  
15               cDNA insert of clone vq8\_1 deposited with the ATCC under accession number PTA-368;
- (f)     a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vq8\_1 deposited with the ATCC under accession number PTA-368;
- 20               (g)     a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vq8\_1 deposited with the ATCC under accession number PTA-368;
- (h)     a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:84;
- (i)     a polynucleotide encoding a protein comprising a fragment of the  
25               amino acid sequence of SEQ ID NO:84 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:84;
- (j)     a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k)     a polynucleotide which encodes a species homologue of the protein  
30               of (h) or (i) above ;
- (l)     a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:83.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:83 from nucleotide 119 to nucleotide 475; the nucleotide sequence of SEQ ID NO:83 from nucleotide 185 to nucleotide 475; the nucleotide sequence of the full-length protein coding sequence of clone vq8\_1 deposited with the ATCC under accession number PTA-368; or the nucleotide sequence of a mature protein coding sequence of clone vq8\_1 deposited with the ATCC under accession number PTA-368. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vq8\_1 deposited with the ATCC under accession number PTA-368. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:84 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:84, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:84 having biological activity, the fragment comprising the amino acid sequence from amino acid 54 to amino acid 63 of SEQ ID NO:84.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:83.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:83, but excluding the poly(A) tail at the 3' end of SEQ ID NO:83; and
    - (ab) the nucleotide sequence of the cDNA insert of clone vq8\_1 deposited with the ATCC under accession number PTA-368;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

5 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:83, but excluding the poly(A) tail at the 3' end of SEQ ID NO:83; and

10 (bb) the nucleotide sequence of the cDNA insert of clone vq8\_1 deposited with the ATCC under accession number PTA-368;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

15 (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:83, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:83 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:83, but  
20 excluding the poly(A) tail at the 3' end of SEQ ID NO:83. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:83 from nucleotide 119 to nucleotide 475, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:83 from nucleotide 119 to nucleotide 475, to a nucleotide  
25 sequence corresponding to the 3' end of said sequence of SEQ ID NO:83 from nucleotide 119 to nucleotide 475. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:83 from nucleotide 185 to nucleotide 475, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:83 from  
30 nucleotide 185 to nucleotide 475, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:83 from nucleotide 185 to nucleotide 475.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:84;
  - 5 (b) a fragment of the amino acid sequence of SEQ ID NO:84, the fragment comprising eight contiguous amino acids of SEQ ID NO:84; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone vq8\_1 deposited with the ATCC under accession number PTA-368;
- the protein being substantially free from other mammalian proteins. Preferably such
- 10 protein comprises the amino acid sequence of SEQ ID NO:84. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:84 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:84, or a protein comprising a fragment of the amino acid sequence of SEQ
- 15 ID NO:84 having biological activity, the fragment comprising the amino acid sequence from amino acid 54 to amino acid 63 of SEQ ID NO:84.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID
- 20 NO:85;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:85 from nucleotide 90 to nucleotide 323;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:85 from nucleotide 141 to nucleotide 323;
- 25 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vq9\_1 deposited with the ATCC under accession number PTA-368;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vq9\_1 deposited with the ATCC under accession number
- 30 PTA-368;

- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vq9\_1 deposited with the ATCC under accession number PTA-368;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vq9\_1 deposited with the ATCC under accession number PTA-368;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:86;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:86 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:86;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:85.
- Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:85 from nucleotide 90 to nucleotide 323; the nucleotide sequence of SEQ ID NO:85 from nucleotide 141 to nucleotide 323; the nucleotide sequence of the full-length protein coding sequence of clone vq9\_1 deposited with the ATCC under accession number PTA-368; or the nucleotide sequence of a mature protein coding sequence of clone vq9\_1 deposited with the ATCC under accession number PTA-368. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vq9\_1 deposited with the ATCC under accession number PTA-368. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:86 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:86, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of

SEQ ID NO:86 having biological activity, the fragment comprising the amino acid sequence from amino acid 34 to amino acid 43 of SEQ ID NO:86.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:85.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:85, but excluding the poly(A) tail at the 3' end of SEQ ID NO:85; and

(ab) the nucleotide sequence of the cDNA insert of clone vq9\_1 deposited with the ATCC under accession number PTA-368;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:85, but excluding the poly(A) tail at the 3' end of SEQ ID NO:85; and

(bb) the nucleotide sequence of the cDNA insert of clone vq9\_1 deposited with the ATCC under accession number PTA-368;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:85, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:85 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:85, but  
5 excluding the poly(A) tail at the 3' end of SEQ ID NO:85. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:85 from nucleotide 90 to nucleotide 323, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:85 from nucleotide 90 to nucleotide 323, to a nucleotide  
10 sequence corresponding to the 3' end of said sequence of SEQ ID NO:85 from nucleotide 90 to nucleotide 323. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:85 from nucleotide 141 to nucleotide 323, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:85 from  
15 nucleotide 141 to nucleotide 323, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:85 from nucleotide 141 to nucleotide 323.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 20 (a) the amino acid sequence of SEQ ID NO:86;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:86, the fragment comprising eight contiguous amino acids of SEQ ID NO:86; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone vq9\_1 deposited with the ATCC under accession number PTA-368;
- 25 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:86. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:86 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids  
30 of SEQ ID NO:86, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:86 having biological activity, the fragment comprising the amino acid sequence from amino acid 34 to amino acid 43 of SEQ ID NO:86.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:87;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:87 from nucleotide 18 to nucleotide 452;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:87 from nucleotide 72 to nucleotide 452;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vq10\_1 deposited with the ATCC under  
10 accession number PTA-368;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vq10\_1 deposited with the ATCC under accession number PTA-368;
- 15 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vq10\_1 deposited with the ATCC under accession number PTA-368;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vq10\_1 deposited with the ATCC under accession number PTA-  
20 368;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:88;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88 having biological activity, the fragment  
25 comprising eight contiguous amino acids of SEQ ID NO:88;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 30 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and



(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:87.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:87 from nucleotide 18 to nucleotide 452; the nucleotide sequence of SEQ ID NO:87 from nucleotide 72 to nucleotide 452; the nucleotide sequence of the full-length protein coding sequence of clone vq10\_1 deposited with the ATCC under accession number PTA-368; or the nucleotide sequence of a mature protein coding sequence of clone vq10\_1 deposited with the ATCC under accession number PTA-368. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vq10\_1 deposited with the ATCC under accession number PTA-368. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:88, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88 having biological activity, the fragment comprising the amino acid sequence from amino acid 67 to amino acid 76 of SEQ ID NO:88.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:87.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:87, but excluding the poly(A) tail at the 3' end of SEQ ID NO:87; and
    - (ab) the nucleotide sequence of the cDNA insert of clone vq10\_1 deposited with the ATCC under accession number PTA-368;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

5 and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

10 (ba) SEQ ID NO:87, but excluding the poly(A) tail at the 3' end of SEQ ID NO:87; and

(bb) the nucleotide sequence of the cDNA insert of clone vq10\_1 deposited with the ATCC under accession number PTA-368;

15 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a  
20 nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:87, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:87 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:87, but excluding the poly(A) tail at the 3' end of SEQ ID NO:87. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence  
25 corresponding to the cDNA sequence of SEQ ID NO:87 from nucleotide 18 to nucleotide 452, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:87 from nucleotide 18 to nucleotide 452, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:87 from nucleotide 18 to nucleotide 452. Also preferably the polynucleotide isolated according to the above  
30 process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:87 from nucleotide 72 to nucleotide 452, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:87 from

nucleotide 72 to nucleotide 452, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:87 from nucleotide 72 to nucleotide 452.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group  
5 consisting of:

- (a) the amino acid sequence of SEQ ID NO:88;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:88, the fragment comprising eight contiguous amino acids of SEQ ID NO:88; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone  
10 vq10\_1 deposited with the ATCC under accession number PTA-368;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:88. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88 having biological activity, the fragment preferably  
15 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:88, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88 having biological activity, the fragment comprising the amino acid sequence from amino acid 67 to amino acid 76 of SEQ ID NO:88.

In one embodiment, the present invention provides a composition comprising an  
20 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:89;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:89 from nucleotide 196 to nucleotide 378;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID  
25 NO:89 from nucleotide 262 to nucleotide 378;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vq13\_1 deposited with the ATCC under accession number PTA-368;
- (e) a polynucleotide encoding the full-length protein encoded by the  
30 cDNA insert of clone vq13\_1 deposited with the ATCC under accession number PTA-368;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vq13\_1 deposited with the ATCC under accession number PTA-368;

5 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vq13\_1 deposited with the ATCC under accession number PTA-368;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:90;

10 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:90 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:90;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

15 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

20 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:89.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:89 from nucleotide 196 to nucleotide 378; the nucleotide sequence of SEQ ID NO:89 from nucleotide 262 to nucleotide 378; the nucleotide sequence of the full-length protein coding sequence of clone vq13\_1 deposited with the ATCC under accession number PTA-25 368; or the nucleotide sequence of a mature protein coding sequence of clone vq13\_1 deposited with the ATCC under accession number PTA-368. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vq13\_1 deposited with the ATCC under accession number PTA-368. In further preferred embodiments, the present invention provides a polynucleotide 30 encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:90 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:90, or a

polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:90 having biological activity, the fragment comprising the amino acid sequence from amino acid 25 to amino acid 34 of SEQ ID NO:90.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ  
5 ID NO:89.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:  
(i) preparing one or more polynucleotide probes that hybridize  
10 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:89, but excluding the poly(A) tail at the 3' end of SEQ ID NO:89; and

(ab) the nucleotide sequence of the cDNA insert of clone  
15 vq13\_1 deposited with the ATCC under accession number PTA-368;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the  
20 probe(s);

and

(b) a process comprising the steps of:  
(i) preparing one or more polynucleotide primers that hybridize  
25 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:89, but excluding the poly(A) tail at the 3' end of SEQ ID NO:89; and

(bb) the nucleotide sequence of the cDNA insert of clone  
30 vq13\_1 deposited with the ATCC under accession number PTA-368;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:89, and  
5 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:89 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:89, but excluding the poly(A) tail at the 3' end of SEQ ID NO:89. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:89 from nucleotide 196 to nucleotide  
10 378, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:89 from nucleotide 196 to nucleotide 378, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:89 from nucleotide 196 to nucleotide 378. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID  
15 NO:89 from nucleotide 262 to nucleotide 378, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:89 from nucleotide 262 to nucleotide 378, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:89 from nucleotide 262 to nucleotide 378.

In other embodiments, the present invention provides a composition comprising  
20 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:90;
- (b) a fragment of the amino acid sequence of SEQ ID NO:90, the fragment comprising eight contiguous amino acids of SEQ ID NO:90; and
- 25 (c) the amino acid sequence encoded by the cDNA insert of clone vq13\_1 deposited with the ATCC under accession number PTA-368;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:90. In further preferred  
30 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:90 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:90, or a protein comprising a fragment of the amino acid sequence of SEQ

ID NO:90 having biological activity, the fragment comprising the amino acid sequence from amino acid 25 to amino acid 34 of SEQ ID NO:90.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 5                   (a)     a polynucleotide comprising the nucleotide sequence of SEQ ID NO:91;
- (b)     a polynucleotide comprising the nucleotide sequence of SEQ ID NO:91 from nucleotide 35 to nucleotide 718;
- (c)     a polynucleotide comprising the nucleotide sequence of SEQ ID  
10               NO:91 from nucleotide 173 to nucleotide 718;
- (d)     a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vq16\_1 deposited with the ATCC under accession number PTA-368;
- (e)     a polynucleotide encoding the full-length protein encoded by the  
15               cDNA insert of clone vq16\_1 deposited with the ATCC under accession number PTA-368;
- (f)     a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vq16\_1 deposited with the ATCC under accession number PTA-368;
- 20               (g)     a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vq16\_1 deposited with the ATCC under accession number PTA-368;
- (h)     a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:92;
- 25               (i)     a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:92 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:92;
- (j)     a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- 30               (k)     a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:91.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:91 from nucleotide 35 to nucleotide 718; the nucleotide sequence of SEQ ID NO:91 from nucleotide 173 to nucleotide 718; the nucleotide sequence of the full-length protein coding sequence of clone vq16\_1 deposited with the ATCC under accession number PTA-368; or the nucleotide sequence of a mature protein coding sequence of clone vq16\_1 deposited with the ATCC under accession number PTA-368. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vq16\_1 deposited with the ATCC under accession number PTA-368. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:92 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:92, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:92 having biological activity, the fragment comprising the amino acid sequence from amino acid 109 to amino acid 118 of SEQ ID NO:92.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:91.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:91, but excluding the poly(A) tail at the 3' end of SEQ ID NO:91; and



- (ab) the nucleotide sequence of the cDNA insert of clone  
vq16\_1 deposited with the ATCC under accession number PTA-368;  
(ii) hybridizing said probe(s) to human genomic DNA in  
conditions at least as stringent as 4X SSC at 50 degrees C; and  
5 (iii) isolating the DNA polynucleotides detected with the  
probe(s);

and

- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that hybridize  
10 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the  
group consisting of:
- (ba) SEQ ID NO:91, but excluding the poly(A) tail at the  
3' end of SEQ ID NO:91; and
- (bb) the nucleotide sequence of the cDNA insert of clone  
15 vq16\_1 deposited with the ATCC under accession number PTA-  
368;
- (ii) hybridizing said primer(s) to human genomic DNA in  
conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and  
20 (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a  
nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:91, and  
extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID  
NO:91 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:91, but  
25 excluding the poly(A) tail at the 3' end of SEQ ID NO:91. Also preferably the  
polynucleotide isolated according to the above process comprises a nucleotide sequence  
corresponding to the cDNA sequence of SEQ ID NO:91 from nucleotide 35 to nucleotide  
718, and extending contiguously from a nucleotide sequence corresponding to the 5' end  
of said sequence of SEQ ID NO:91 from nucleotide 35 to nucleotide 718, to a nucleotide  
30 sequence corresponding to the 3' end of said sequence of SEQ ID NO:91 from nucleotide  
35 to nucleotide 718. Also preferably the polynucleotide isolated according to the above  
process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID

NO:91 from nucleotide 173 to nucleotide 718, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:91 from nucleotide 173 to nucleotide 718, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:91 from nucleotide 173 to nucleotide 718.

5 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:92;
- (b) a fragment of the amino acid sequence of SEQ ID NO:92, the  
10 fragment comprising eight contiguous amino acids of SEQ ID NO:92; and
- (c) the amino acid sequence encoded by the cDNA insert of clone  
vq16\_1 deposited with the ATCC under accession number PTA-368;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:92. In further preferred  
15 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:92 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:92, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:92 having biological activity, the fragment comprising the amino acid sequence  
20 from amino acid 109 to amino acid 118 of SEQ ID NO:92.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID  
NO:93;
- 25 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID  
NO:93 from nucleotide 1 to nucleotide 762;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID  
NO:93 from nucleotide 70 to nucleotide 762;
- (d) a polynucleotide comprising the nucleotide sequence of the full-  
30 length protein coding sequence of clone vq19\_1 deposited with the ATCC under  
accession number PTA-368;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vq19\_1 deposited with the ATCC under accession number PTA-368;

5 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vq19\_1 deposited with the ATCC under accession number PTA-368;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vq19\_1 deposited with the ATCC under accession number PTA-368;

10 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:94;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:94 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:94;

15 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

20 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:93.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID  
25 NO:93 from nucleotide 1 to nucleotide 762; the nucleotide sequence of SEQ ID NO:93 from nucleotide 70 to nucleotide 762; the nucleotide sequence of the full-length protein coding sequence of clone vq19\_1 deposited with the ATCC under accession number PTA-368; or the nucleotide sequence of a mature protein coding sequence of clone vq19\_1 deposited with the ATCC under accession number PTA-368. In other preferred  
30 embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vq19\_1 deposited with the ATCC under accession number PTA-368. In further preferred embodiments, the present invention provides a polynucleotide

encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:94 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:94, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of  
5 SEQ ID NO:94 having biological activity, the fragment comprising the amino acid sequence from amino acid 122 to amino acid 131 of SEQ ID NO:94.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:93.

Further embodiments of the invention provide isolated polynucleotides produced  
10 according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

15 (aa) SEQ ID NO:93, but excluding the poly(A) tail at the 3' end of SEQ ID NO:93; and

(ab) the nucleotide sequence of the cDNA insert of clone vq19\_1 deposited with the ATCC under accession number PTA-368;

20 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

25 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

30 (ba) SEQ ID NO:93, but excluding the poly(A) tail at the 3' end of SEQ ID NO:93; and

- (bb) the nucleotide sequence of the cDNA insert of clone vq19\_1 deposited with the ATCC under accession number PTA-368;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- 5 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:93, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID  
10 NO:93 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:93, but excluding the poly(A) tail at the 3' end of SEQ ID NO:93. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:93 from nucleotide 1 to nucleotide 762, and extending contiguously from a nucleotide sequence corresponding to the 5' end  
15 of said sequence of SEQ ID NO:93 from nucleotide 1 to nucleotide 762, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:93 from nucleotide 1 to nucleotide 762. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:93 from nucleotide 70 to nucleotide 762, and extending contiguously from a  
20 nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:93 from nucleotide 70 to nucleotide 762, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:93 from nucleotide 70 to nucleotide 762.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group  
25 consisting of:

- (a) the amino acid sequence of SEQ ID NO:94;
- (b) a fragment of the amino acid sequence of SEQ ID NO:94, the fragment comprising eight contiguous amino acids of SEQ ID NO:94; and
- (c) the amino acid sequence encoded by the cDNA insert of clone  
30 vq19\_1 deposited with the ATCC under accession number PTA-368;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:94. In further preferred

embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:94 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:94, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:94 having biological activity, the fragment comprising the amino acid sequence from amino acid 122 to amino acid 131 of SEQ ID NO:94.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 10 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:95;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:95 from nucleotide 106 to nucleotide 792;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:95 from nucleotide 172 to nucleotide 792;
- 15 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vq20\_1 deposited with the ATCC under accession number PTA-368;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vq20\_1 deposited with the ATCC under accession number  
20 PTA-368;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vq20\_1 deposited with the ATCC under accession number PTA-368;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA  
25 insert of clone vq20\_1 deposited with the ATCC under accession number PTA-368;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:96;
- 30 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:96;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

5 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:95.

10 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:95 from nucleotide 106 to nucleotide 792; the nucleotide sequence of SEQ ID NO:95 from nucleotide 172 to nucleotide 792; the nucleotide sequence of the full-length protein coding sequence of clone vq20\_1 deposited with the ATCC under accession number PTA-368; or the nucleotide sequence of a mature protein coding sequence of clone vq20\_1  
15 deposited with the ATCC under accession number PTA-368. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vq20\_1 deposited with the ATCC under accession number PTA-368. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96  
20 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:96, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96 having biological activity, the fragment comprising the amino acid sequence from amino acid 109 to amino acid 118 of SEQ ID NO:96.

25 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:95.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

30 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- (aa) SEQ ID NO:95, but excluding the poly(A) tail at the 3' end of SEQ ID NO:95; and
- (ab) the nucleotide sequence of the cDNA insert of clone vq20\_1 deposited with the ATCC under accession number PTA-368;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:95, but excluding the poly(A) tail at the 3' end of SEQ ID NO:95; and
- (bb) the nucleotide sequence of the cDNA insert of clone vq20\_1 deposited with the ATCC under accession number PTA-368;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:95, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:95 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:95, but excluding the poly(A) tail at the 3' end of SEQ ID NO:95. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:95 from nucleotide 106 to nucleotide 792, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:95 from nucleotide 106 to nucleotide 792, to a nucleotide



sequence corresponding to the 3' end of said sequence of SEQ ID NO:95 from nucleotide 106 to nucleotide 792. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:95 from nucleotide 172 to nucleotide 792, and extending contiguously from a  
5 nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:95 from nucleotide 172 to nucleotide 792, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:95 from nucleotide 172 to nucleotide 792.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group  
10 consisting of:

- (a) the amino acid sequence of SEQ ID NO:96;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:96, the fragment comprising eight contiguous amino acids of SEQ ID NO:96; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone  
15 vq20\_1 deposited with the ATCC under accession number PTA-368;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:96. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96 having biological activity, the fragment preferably  
20 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:96, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96 having biological activity, the fragment comprising the amino acid sequence from amino acid 109 to amino acid 118 of SEQ ID NO:96.

In one embodiment, the present invention provides a composition comprising an  
25 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:97;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:97 from nucleotide 40 to nucleotide 315;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID  
30 NO:97 from nucleotide 124 to nucleotide 315;

- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vq21\_1 deposited with the ATCC under accession number PTA-368;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vq21\_1 deposited with the ATCC under accession number PTA-368;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vq21\_1 deposited with the ATCC under accession number PTA-368;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vq21\_1 deposited with the ATCC under accession number PTA-368;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:98;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:98 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:98;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:97.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:97 from nucleotide 40 to nucleotide 315; the nucleotide sequence of SEQ ID NO:97 from nucleotide 124 to nucleotide 315; the nucleotide sequence of the full-length protein coding sequence of clone vq21\_1 deposited with the ATCC under accession number PTA-368; or the nucleotide sequence of a mature protein coding sequence of clone vq21\_1 deposited with the ATCC under accession number PTA-368. In other preferred

embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vq21\_1 deposited with the ATCC under accession number PTA-368. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:98 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:98, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:98 having biological activity, the fragment comprising the amino acid sequence from amino acid 41 to amino acid 50 of SEQ ID NO:98.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:97.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
    - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
      - (aa) SEQ ID NO:97, but excluding the poly(A) tail at the 3' end of SEQ ID NO:97; and
      - (ab) the nucleotide sequence of the cDNA insert of clone vq21\_1 deposited with the ATCC under accession number PTA-368;
      - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
      - (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
    - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- (ba) SEQ ID NO:97, but excluding the poly(A) tail at the 3' end of SEQ ID NO:97; and
- (bb) the nucleotide sequence of the cDNA insert of clone vq21\_1 deposited with the ATCC under accession number PTA-368;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).
- 10 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:97, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:97 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:97, but excluding the poly(A) tail at the 3' end of SEQ ID NO:97. Also preferably the
- 15 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:97 from nucleotide 40 to nucleotide 315, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:97 from nucleotide 40 to nucleotide 315, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:97 from nucleotide
- 20 40 to nucleotide 315. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:97 from nucleotide 124 to nucleotide 315, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:97 from nucleotide 124 to nucleotide 315, to a nucleotide sequence corresponding to the 3' end of
- 25 said sequence of SEQ ID NO:97 from nucleotide 124 to nucleotide 315.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:98;
- 30 (b) a fragment of the amino acid sequence of SEQ ID NO:98, the fragment comprising eight contiguous amino acids of SEQ ID NO:98; and

(c) the amino acid sequence encoded by the cDNA insert of clone  
vq21\_1 deposited with the ATCC under accession number PTA-368;  
the protein being substantially free from other mammalian proteins. Preferably such  
protein comprises the amino acid sequence of SEQ ID NO:98. In further preferred  
5 embodiments, the present invention provides a protein comprising a fragment of the amino  
acid sequence of SEQ ID NO:98 having biological activity, the fragment preferably  
comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids  
of SEQ ID NO:98, or a protein comprising a fragment of the amino acid sequence of SEQ  
ID NO:98 having biological activity, the fragment comprising the amino acid sequence  
10 from amino acid 41 to amino acid 50 of SEQ ID NO:98.

In one embodiment, the present invention provides a composition comprising an  
isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID  
NO:99;
- 15 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID  
NO:99 from nucleotide 70 to nucleotide 699;
- (c) a polynucleotide comprising the nucleotide sequence of the full-  
length protein coding sequence of clone vr2\_1 deposited with the ATCC under  
accession number PTA-368;
- 20 (d) a polynucleotide encoding the full-length protein encoded by the  
cDNA insert of clone vr2\_1 deposited with the ATCC under accession number  
PTA-368;
- (e) a polynucleotide comprising the nucleotide sequence of a mature  
protein coding sequence of clone vr2\_1 deposited with the ATCC under accession  
25 number PTA-368;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA  
insert of clone vr2\_1 deposited with the ATCC under accession number PTA-368;
- (g) a polynucleotide encoding a protein comprising the amino acid  
sequence of SEQ ID NO:100;
- 30 (h) a polynucleotide encoding a protein comprising a fragment of the  
amino acid sequence of SEQ ID NO:100 having biological activity, the fragment  
comprising eight contiguous amino acids of SEQ ID NO:100;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

5 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:99.

10 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:99 from nucleotide 70 to nucleotide 699; the nucleotide sequence of the full-length protein coding sequence of clone vr2\_1 deposited with the ATCC under accession number PTA-368; or the nucleotide sequence of a mature protein coding sequence of clone vr2\_1 deposited with the ATCC under accession number PTA-368. In other preferred  
15 embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vr2\_1 deposited with the ATCC under accession number PTA-368. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:100 having biological activity, the fragment preferably comprising eight (more preferably  
20 twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:100, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:100 having biological activity, the fragment comprising the amino acid sequence from amino acid 100 to amino acid 109 of SEQ ID NO:100.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ  
25 ID NO:99.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

30 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:99, but excluding the poly(A) tail at the 3' end of SEQ ID NO:99; and

(ab) the nucleotide sequence of the cDNA insert of clone vr2\_1 deposited with the ATCC under accession number PTA-368;

5 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

10 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

15 (ba) SEQ ID NO:99, but excluding the poly(A) tail at the 3' end of SEQ ID NO:99; and

(bb) the nucleotide sequence of the cDNA insert of clone vr2\_1 deposited with the ATCC under accession number PTA-368;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

20 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:99, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID  
25 NO:99 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:99, but excluding the poly(A) tail at the 3' end of SEQ ID NO:99. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:99 from nucleotide 70 to nucleotide 699, and extending contiguously from a nucleotide sequence corresponding to the 5' end  
30 of said sequence of SEQ ID NO:99 from nucleotide 70 to nucleotide 699, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:99 from nucleotide 70 to nucleotide 699.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:100;
  - 5 (b) a fragment of the amino acid sequence of SEQ ID NO:100, the fragment comprising eight contiguous amino acids of SEQ ID NO:100; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone vr2\_1 deposited with the ATCC under accession number PTA-368;
- the protein being substantially free from other mammalian proteins. Preferably such
- 10 protein comprises the amino acid sequence of SEQ ID NO:100. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:100 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:100, or a protein comprising a fragment of the amino acid sequence of SEQ
- 15 ID NO:100 having biological activity, the fragment comprising the amino acid sequence from amino acid 100 to amino acid 109 of SEQ ID NO:100.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID
- 20 NO:101;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:101 from nucleotide 170 to nucleotide 394;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:101 from nucleotide 227 to nucleotide 394;
- 25 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vc69\_1 deposited with the ATCC under accession number PTA-1075;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vc69\_1 deposited with the ATCC under accession number
- 30 PTA-1075;



(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vc69\_1 deposited with the ATCC under accession number PTA-1075;

5 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vc69\_1 deposited with the ATCC under accession number PTA-1075;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:102;

10 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:102 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:102;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

15 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

20 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:101.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:101 from nucleotide 170 to nucleotide 394; the nucleotide sequence of SEQ ID NO:101 from nucleotide 227 to nucleotide 394; the nucleotide sequence of the full-length protein coding sequence of clone vc69\_1 deposited with the ATCC under accession  
25 number PTA-1075; or the nucleotide sequence of a mature protein coding sequence of clone vc69\_1 deposited with the ATCC under accession number PTA-1075. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vc69\_1 deposited with the ATCC under accession number PTA-1075. In further preferred embodiments, the present invention provides a  
30 polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:102 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID

NO:102, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:102 having biological activity, the fragment comprising the amino acid sequence from amino acid 32 to amino acid 41 of SEQ ID NO:102.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ  
5 ID NO:101.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
    - (i) preparing one or more polynucleotide probes that hybridize  
10 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
      - (aa) SEQ ID NO:101, but excluding the poly(A) tail at the 3' end of SEQ ID NO:101; and
      - (ab) the nucleotide sequence of the cDNA insert of clone  
15 vc69\_1 deposited with the ATCC under accession number PTA-1075;
    - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
    - (iii) isolating the DNA polynucleotides detected with the  
20 probe(s);
- and
- (b) a process comprising the steps of:
    - (i) preparing one or more polynucleotide primers that hybridize  
25 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
      - (ba) SEQ ID NO:101, but excluding the poly(A) tail at the 3' end of SEQ ID NO:101; and
      - (bb) the nucleotide sequence of the cDNA insert of clone  
30 vc69\_1 deposited with the ATCC under accession number PTA-1075;
    - (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:101, and  
5 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:101 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:101, but excluding the poly(A) tail at the 3' end of SEQ ID NO:101. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:101 from nucleotide 170 to  
10 nucleotide 394, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:101 from nucleotide 170 to nucleotide 394, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:101 from nucleotide 170 to nucleotide 394. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the  
15 cDNA sequence of SEQ ID NO:101 from nucleotide 227 to nucleotide 394, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:101 from nucleotide 227 to nucleotide 394, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:101 from nucleotide 227 to nucleotide 394.

20 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:102;
- (b) a fragment of the amino acid sequence of SEQ ID NO:102, the  
25 fragment comprising eight contiguous amino acids of SEQ ID NO:102; and
- (c) the amino acid sequence encoded by the cDNA insert of clone vc69\_1 deposited with the ATCC under accession number PTA-1075;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:102. In further preferred  
30 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:102 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids

of SEQ ID NO:102, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:102 having biological activity, the fragment comprising the amino acid sequence from amino acid 32 to amino acid 41 of SEQ ID NO:102.

In one embodiment, the present invention provides a composition comprising an  
5 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:103;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:103 from nucleotide 43 to nucleotide 198;
- 10 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:103 from nucleotide 85 to nucleotide 198;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vc71\_1 deposited with the ATCC under accession number PTA-1075;
- 15 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vc71\_1 deposited with the ATCC under accession number PTA-1075;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vc71\_1 deposited with the ATCC under  
20 accession number PTA-1075;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vc71\_1 deposited with the ATCC under accession number PTA-1075;
- (h) a polynucleotide encoding a protein comprising the amino acid  
25 sequence of SEQ ID NO:104;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:104 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:104;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of  
30 (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:103.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:103 from nucleotide 43 to nucleotide 198; the nucleotide sequence of SEQ ID NO:103 from nucleotide 85 to nucleotide 198; the nucleotide sequence of the full-length protein coding sequence of clone vc71\_1 deposited with the ATCC under accession number PTA-1075; or the nucleotide sequence of a mature protein coding sequence of clone vc71\_1 deposited with the ATCC under accession number PTA-1075. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vc71\_1 deposited with the ATCC under accession number PTA-1075. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:104 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:104, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:104 having biological activity, the fragment comprising the amino acid sequence from amino acid 21 to amino acid 30 of SEQ ID NO:104.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:103.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (aa) SEQ ID NO:103, but excluding the poly(A) tail at the 3' end of SEQ ID NO:103; and

- (ab) the nucleotide sequence of the cDNA insert of clone vc71\_1 deposited with the ATCC under accession number PTA-1075;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 5 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that hybridize
- 10 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:103, but excluding the poly(A) tail at the 3' end of SEQ ID NO:103; and
- (bb) the nucleotide sequence of the cDNA insert of clone
- 15 vc71\_1 deposited with the ATCC under accession number PTA-1075;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- 20 (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:103, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:103 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:103, but

25 excluding the poly(A) tail at the 3' end of SEQ ID NO:103. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:103 from nucleotide 43 to nucleotide 198, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:103 from nucleotide 43 to nucleotide 198, to a nucleotide

30 sequence corresponding to the 3' end of said sequence of SEQ ID NO:103 from nucleotide 43 to nucleotide 198. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID

NO:103 from nucleotide 85 to nucleotide 198, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:103 from nucleotide 85 to nucleotide 198, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:103 from nucleotide 85 to nucleotide 198.

5 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:104;
- (b) a fragment of the amino acid sequence of SEQ ID NO:104, the  
10 fragment comprising eight contiguous amino acids of SEQ ID NO:104; and
- (c) the amino acid sequence encoded by the cDNA insert of clone  
vc71\_1 deposited with the ATCC under accession number PTA-1075;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:104. In further preferred  
15 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:104 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:104, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:104 having biological activity, the fragment comprising the amino acid sequence  
20 from amino acid 21 to amino acid 30 of SEQ ID NO:104.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID  
NO:105;
- 25 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID  
NO:105 from nucleotide 260 to nucleotide 1552;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID  
NO:105 from nucleotide 335 to nucleotide 1552;
- (d) a polynucleotide comprising the nucleotide sequence of the full-  
30 length protein coding sequence of clone vo27\_1 deposited with the ATCC under  
accession number PTA-1075;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vo27\_1 deposited with the ATCC under accession number PTA-1075;

5 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo27\_1 deposited with the ATCC under accession number PTA-1075;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vo27\_1 deposited with the ATCC under accession number PTA-1075;

10 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:106;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:106 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:106;

15 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

20 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:105.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID  
25 NO:105 from nucleotide 260 to nucleotide 1552; the nucleotide sequence of SEQ ID NO:105 from nucleotide 335 to nucleotide 1552; the nucleotide sequence of the full-length protein coding sequence of clone vo27\_1 deposited with the ATCC under accession number PTA-1075; or the nucleotide sequence of a mature protein coding sequence of clone vo27\_1 deposited with the ATCC under accession number PTA-1075. In other  
30 preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vo27\_1 deposited with the ATCC under accession number PTA-1075. In further preferred embodiments, the present invention provides a



polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:106 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:106, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:106 having biological activity, the fragment comprising the amino acid sequence from amino acid 210 to amino acid 219 of SEQ ID NO:106.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:105.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:105, but excluding the poly(A) tail at the 3' end of SEQ ID NO:105; and

(ab) the nucleotide sequence of the cDNA insert of clone vo27\_1 deposited with the ATCC under accession number PTA-1075;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:105, but excluding the poly(A) tail at the 3' end of SEQ ID NO:105; and

- (bb) the nucleotide sequence of the cDNA insert of clone vo27\_1 deposited with the ATCC under accession number PTA-1075;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- 5 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:105, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:105 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:105, but excluding the poly(A) tail at the 3' end of SEQ ID NO:105. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:105 from nucleotide 260 to nucleotide 1552, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:105 from nucleotide 260 to nucleotide 1552, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:105 from nucleotide 260 to nucleotide 1552. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:105 from nucleotide 335 to nucleotide 1552, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:105 from nucleotide 335 to nucleotide 1552, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:105 from nucleotide 335 to nucleotide 1552.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:106;
- (b) a fragment of the amino acid sequence of SEQ ID NO:106, the fragment comprising eight contiguous amino acids of SEQ ID NO:106; and
- 30 (c) the amino acid sequence encoded by the cDNA insert of clone vo27\_1 deposited with the ATCC under accession number PTA-1075;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:106. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:106 having biological activity, the fragment preferably  
5 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:106, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:106 having biological activity, the fragment comprising the amino acid sequence from amino acid 210 to amino acid 219 of SEQ ID NO:106.

In one embodiment, the present invention provides a composition comprising an  
10 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:107;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:107 from nucleotide 15 to nucleotide 320;
- 15 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:107 from nucleotide 72 to nucleotide 320;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vo31\_1 deposited with the ATCC under accession number PTA-1075;
- 20 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vo31\_1 deposited with the ATCC under accession number PTA-1075;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo31\_1 deposited with the ATCC under  
25 accession number PTA-1075;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vo31\_1 deposited with the ATCC under accession number PTA-1075;
- 30 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:108;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:108 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:108;

5 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

10 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:107.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:107 from nucleotide 15 to nucleotide 320; the nucleotide sequence of SEQ ID NO:107  
15 from nucleotide 72 to nucleotide 320; the nucleotide sequence of the full-length protein coding sequence of clone vo31\_1 deposited with the ATCC under accession number PTA-1075; or the nucleotide sequence of a mature protein coding sequence of clone vo31\_1 deposited with the ATCC under accession number PTA-1075. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by  
20 the cDNA insert of clone vo31\_1 deposited with the ATCC under accession number PTA-1075. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:108 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:108, or a  
25 polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:108 having biological activity, the fragment comprising the amino acid sequence from amino acid 46 to amino acid 55 of SEQ ID NO:108.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:107.

30 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (aa) SEQ ID NO:107, but excluding the poly(A) tail at the 3' end of SEQ ID NO:107; and

(ab) the nucleotide sequence of the cDNA insert of clone vo31\_1 deposited with the ATCC under accession number PTA-1075;

10 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

15 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:107, but excluding the poly(A) tail at the 3' end of SEQ ID NO:107; and

20 (bb) the nucleotide sequence of the cDNA insert of clone vo31\_1 deposited with the ATCC under accession number PTA-1075;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

25 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:107, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID  
30 NO:107 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:107, but excluding the poly(A) tail at the 3' end of SEQ ID NO:107. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence

corresponding to the cDNA sequence of SEQ ID NO:107 from nucleotide 15 to nucleotide 320, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:107 from nucleotide 15 to nucleotide 320, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:107 from nucleotide 15 to nucleotide 320. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:107 from nucleotide 72 to nucleotide 320, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:107 from nucleotide 72 to nucleotide 320, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:107 from nucleotide 72 to nucleotide 320.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:108;
- (b) a fragment of the amino acid sequence of SEQ ID NO:108, the fragment comprising eight contiguous amino acids of SEQ ID NO:108; and
- (c) the amino acid sequence encoded by the cDNA insert of clone vo31\_1 deposited with the ATCC under accession number PTA-1075;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:108. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:108 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:108, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:108 having biological activity, the fragment comprising the amino acid sequence from amino acid 46 to amino acid 55 of SEQ ID NO:108.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:109;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:109 from nucleotide 38 to nucleotide 1255;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:109 from nucleotide 86 to nucleotide 1255;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vo32\_1 deposited with the ATCC under accession number PTA-1075;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vo32\_1 deposited with the ATCC under accession number PTA-1075;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo32\_1 deposited with the ATCC under accession number PTA-1075;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vo32\_1 deposited with the ATCC under accession number PTA-1075;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:110;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:110 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:110;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:109.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:109 from nucleotide 38 to nucleotide 1255; the nucleotide sequence of SEQ ID NO:109 from nucleotide 86 to nucleotide 1255; the nucleotide sequence of the full-length protein coding sequence of clone vo32\_1 deposited with the ATCC under accession

number PTA-1075; or the nucleotide sequence of a mature protein coding sequence of clone vo32\_1 deposited with the ATCC under accession number PTA-1075. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vo32\_1 deposited with the ATCC under accession  
5 number PTA-1075. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:110 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:110, or a polynucleotide encoding a protein comprising a fragment of the amino acid  
10 sequence of SEQ ID NO:110 having biological activity, the fragment comprising the amino acid sequence from amino acid 198 to amino acid 207 of SEQ ID NO:110.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:109.

Further embodiments of the invention provide isolated polynucleotides produced  
15 according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

20 (aa) SEQ ID NO:109, but excluding the poly(A) tail at the 3' end of SEQ ID NO:109; and

(ab) the nucleotide sequence of the cDNA insert of clone vo32\_1 deposited with the ATCC under accession number PTA-1075;

25 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

30 (b) a process comprising the steps of:



(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (ba) SEQ ID NO:109, but excluding the poly(A) tail at the 3' end of SEQ ID NO:109; and

(bb) the nucleotide sequence of the cDNA insert of clone vo32\_1 deposited with the ATCC under accession number PTA-1075;

10 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:109, and  
15 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:109 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:109, but excluding the poly(A) tail at the 3' end of SEQ ID NO:109. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:109 from nucleotide  
20 1255, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:109 from nucleotide 38 to nucleotide 1255, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:109 from nucleotide 38 to nucleotide 1255. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID  
25 NO:109 from nucleotide 86 to nucleotide 1255, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:109 from nucleotide 86 to nucleotide 1255, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:109 from nucleotide 86 to nucleotide 1255.

In other embodiments, the present invention provides a composition comprising  
30 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:110;

(b) a fragment of the amino acid sequence of SEQ ID NO:110, the fragment comprising eight contiguous amino acids of SEQ ID NO:110; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo32\_1 deposited with the ATCC under accession number PTA-1075;

5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:110. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:110 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids  
10 of SEQ ID NO:110, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:110 having biological activity, the fragment comprising the amino acid sequence from amino acid 198 to amino acid 207 of SEQ ID NO:110.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

15 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:111;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:111 from nucleotide 80 to nucleotide 1276;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID  
20 NO:111 from nucleotide 131 to nucleotide 1276;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vo33\_1 deposited with the ATCC under accession number PTA-1075;

(e) a polynucleotide encoding the full-length protein encoded by the  
25 cDNA insert of clone vo33\_1 deposited with the ATCC under accession number PTA-1075;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo33\_1 deposited with the ATCC under accession number PTA-1075;

(g) a polynucleotide encoding a mature protein encoded by the cDNA  
30 insert of clone vo33\_1 deposited with the ATCC under accession number PTA-1075;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:112;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:112 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:112;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:111.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:111 from nucleotide 80 to nucleotide 1276; the nucleotide sequence of SEQ ID NO:111 from nucleotide 131 to nucleotide 1276; the nucleotide sequence of the full-length protein coding sequence of clone vo33\_1 deposited with the ATCC under accession number PTA-1075; or the nucleotide sequence of a mature protein coding sequence of clone vo33\_1 deposited with the ATCC under accession number PTA-1075. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vo33\_1 deposited with the ATCC under accession number PTA-1075. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:112 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:112, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:112 having biological activity, the fragment comprising the amino acid sequence from amino acid 194 to amino acid 203 of SEQ ID NO:112.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:111.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:111, but excluding the poly(A) tail at the 3' end of SEQ ID NO:111; and

(ab) the nucleotide sequence of the cDNA insert of clone vo33\_1 deposited with the ATCC under accession number PTA-1075;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:111, but excluding the poly(A) tail at the 3' end of SEQ ID NO:111; and

(bb) the nucleotide sequence of the cDNA insert of clone vo33\_1 deposited with the ATCC under accession number PTA-1075;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:111, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID

NO:111 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:111, but excluding the poly(A) tail at the 3' end of SEQ ID NO:111. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:111 from nucleotide 80 to nucleotide 1276, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:111 from nucleotide 80 to nucleotide 1276, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:111 from nucleotide 80 to nucleotide 1276. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:111 from nucleotide 131 to nucleotide 1276, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:111 from nucleotide 131 to nucleotide 1276, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:111 from nucleotide 131 to nucleotide 1276.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:112;
- (b) a fragment of the amino acid sequence of SEQ ID NO:112, the fragment comprising eight contiguous amino acids of SEQ ID NO:112; and
- (c) the amino acid sequence encoded by the cDNA insert of clone vo33\_1 deposited with the ATCC under accession number PTA-1075;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:112. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:112 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:112, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:112 having biological activity, the fragment comprising the amino acid sequence from amino acid 194 to amino acid 203 of SEQ ID NO:112.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:113;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:113 from nucleotide 202 to nucleotide 429;
- 5 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:113 from nucleotide 292 to nucleotide 429;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vq23\_1 deposited with the ATCC under accession number PTA-1075;
- 10 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vq23\_1 deposited with the ATCC under accession number PTA-1075;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vq23\_1 deposited with the ATCC under accession number PTA-1075;
- 15 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vq23\_1 deposited with the ATCC under accession number PTA-1075;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:114;
- 20 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:114 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:114;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- 25 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- 30 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:113.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:113 from nucleotide 202 to nucleotide 429; the nucleotide sequence of SEQ ID NO:113 from nucleotide 292 to nucleotide 429; the nucleotide sequence of the full-length protein coding sequence of clone vq23\_1 deposited with the ATCC under accession number PTA-1075; or the nucleotide sequence of a mature protein coding sequence of clone vq23\_1 deposited with the ATCC under accession number PTA-1075. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vq23\_1 deposited with the ATCC under accession number PTA-1075. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:114 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:114, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:114 having biological activity, the fragment comprising the amino acid sequence from amino acid 33 to amino acid 42 of SEQ ID NO:114.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:113.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 20 (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - 25 (aa) SEQ ID NO:113, but excluding the poly(A) tail at the 3' end of SEQ ID NO:113; and
    - (ab) the nucleotide sequence of the cDNA insert of clone vq23\_1 deposited with the ATCC under accession number PTA-1075;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
  - 30 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:113, but excluding the poly(A) tail at the 3' end of SEQ ID NO:113; and

(bb) the nucleotide sequence of the cDNA insert of clone vq23\_1 deposited with the ATCC under accession number PTA-1075;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

15 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:113, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:113 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:113, but excluding the poly(A) tail at the 3' end of SEQ ID NO:113. Also preferably the  
20 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:113 from nucleotide 202 to nucleotide 429, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:113 from nucleotide 202 to nucleotide 429, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:113  
25 from nucleotide 202 to nucleotide 429. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:113 from nucleotide 292 to nucleotide 429, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:113 from nucleotide 292 to nucleotide 429, to a nucleotide sequence  
30 corresponding to the 3' end of said sequence of SEQ ID NO:113 from nucleotide 292 to nucleotide 429.



In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:114;
- 5 (b) a fragment of the amino acid sequence of SEQ ID NO:114, the fragment comprising eight contiguous amino acids of SEQ ID NO:114; and
- (c) the amino acid sequence encoded by the cDNA insert of clone vq23\_1 deposited with the ATCC under accession number PTA-1075;

the protein being substantially free from other mammalian proteins. Preferably such  
10 protein comprises the amino acid sequence of SEQ ID NO:114. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:114 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:114, or a protein comprising a fragment of the amino acid sequence of SEQ  
15 ID NO:114 having biological activity, the fragment comprising the amino acid sequence from amino acid 33 to amino acid 42 of SEQ ID NO:114.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID  
20 NO:115;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:115 from nucleotide 37 to nucleotide 1113;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:115 from nucleotide 88 to nucleotide 1113;
- 25 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vq24\_1 deposited with the ATCC under accession number PTA-1075;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vq24\_1 deposited with the ATCC under accession number  
30 PTA-1075;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vq24\_1 deposited with the ATCC under accession number PTA-1075;

5 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vq24\_1 deposited with the ATCC under accession number PTA-1075;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:116;

10 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:116 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:116;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

15 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

20 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:115.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:115 from nucleotide 37 to nucleotide 1113; the nucleotide sequence of SEQ ID NO:115 from nucleotide 88 to nucleotide 1113; the nucleotide sequence of the full-length protein coding sequence of clone vq24\_1 deposited with the ATCC under accession  
25 number PTA-1075; or the nucleotide sequence of a mature protein coding sequence of clone vq24\_1 deposited with the ATCC under accession number PTA-1075. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vq24\_1 deposited with the ATCC under accession number PTA-1075. In further preferred embodiments, the present invention provides a  
30 polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:116 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID

NO:116, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:116 having biological activity, the fragment comprising the amino acid sequence from amino acid 174 to amino acid 183 of SEQ ID NO:116.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ  
5 ID NO:115.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:  
(i) preparing one or more polynucleotide probes that hybridize  
10 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:115, but excluding the poly(A) tail at the 3' end of SEQ ID NO:115; and  
(ab) the nucleotide sequence of the cDNA insert of clone  
15 vq24\_1 deposited with the ATCC under accession number PTA-1075;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and  
(iii) isolating the DNA polynucleotides detected with the  
20 probe(s);

and

(b) a process comprising the steps of:  
(i) preparing one or more polynucleotide primers that hybridize  
25 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:115, but excluding the poly(A) tail at the 3' end of SEQ ID NO:115; and  
(bb) the nucleotide sequence of the cDNA insert of clone  
30 vq24\_1 deposited with the ATCC under accession number PTA-1075;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:115, and  
5 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:115 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:115, but excluding the poly(A) tail at the 3' end of SEQ ID NO:115. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:115 from nucleotide 37 to nucleotide  
10 1113, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:115 from nucleotide 37 to nucleotide 1113, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:115 from nucleotide 37 to nucleotide 1113. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID  
15 NO:115 from nucleotide 88 to nucleotide 1113, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:115 from nucleotide 88 to nucleotide 1113, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:115 from nucleotide 88 to nucleotide 1113.

In other embodiments, the present invention provides a composition comprising  
20 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:116;
- (b) a fragment of the amino acid sequence of SEQ ID NO:116, the fragment comprising eight contiguous amino acids of SEQ ID NO:116; and
- 25 (c) the amino acid sequence encoded by the cDNA insert of clone vq24\_1 deposited with the ATCC under accession number PTA-1075;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:116. In further preferred  
30 acid sequence of SEQ ID NO:116 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:116, or a protein comprising a fragment of the amino acid sequence of SEQ

ID NO:116 having biological activity, the fragment comprising the amino acid sequence from amino acid 174 to amino acid 183 of SEQ ID NO:116.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 5                   (a)     a polynucleotide comprising the nucleotide sequence of SEQ ID NO:117;
- (b)     a polynucleotide comprising the nucleotide sequence of SEQ ID NO:117 from nucleotide 40 to nucleotide 207;
- (c)     a polynucleotide comprising the nucleotide sequence of SEQ ID  
10               NO:117 from nucleotide 103 to nucleotide 207;
- (d)     a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vq26\_1 deposited with the ATCC under accession number PTA-1075;
- (e)     a polynucleotide encoding the full-length protein encoded by the  
15               cDNA insert of clone vq26\_1 deposited with the ATCC under accession number PTA-1075;
- (f)     a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vq26\_1 deposited with the ATCC under accession number PTA-1075;
- 20               (g)     a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vq26\_1 deposited with the ATCC under accession number PTA-1075;
- (h)     a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:118;
- 25               (i)     a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:118 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:118;
- (j)     a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- 30               (k)     a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:117.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:117 from nucleotide 40 to nucleotide 207; the nucleotide sequence of SEQ ID NO:117 from nucleotide 103 to nucleotide 207; the nucleotide sequence of the full-length protein coding sequence of clone vq26\_1 deposited with the ATCC under accession number PTA-1075; or the nucleotide sequence of a mature protein coding sequence of clone vq26\_1 deposited with the ATCC under accession number PTA-1075. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vq26\_1 deposited with the ATCC under accession number PTA-1075. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:118 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:118, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:118 having biological activity, the fragment comprising the amino acid sequence from amino acid 23 to amino acid 32 of SEQ ID NO:118.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:117.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:117, but excluding the poly(A) tail at the 3' end of SEQ ID NO:117; and

- (ab) the nucleotide sequence of the cDNA insert of clone  
vq26\_1 deposited with the ATCC under accession number PTA-1075;
- (ii) hybridizing said probe(s) to human genomic DNA in  
conditions at least as stringent as 4X SSC at 50 degrees C; and
- 5 (iii) isolating the DNA polynucleotides detected with the  
probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that hybridize  
10 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the  
group consisting of:
- (ba) SEQ ID NO:117, but excluding the poly(A) tail at  
the 3' end of SEQ ID NO:117; and
- (bb) the nucleotide sequence of the cDNA insert of clone  
15 vq26\_1 deposited with the ATCC under accession number PTA-  
1075;
- (ii) hybridizing said primer(s) to human genomic DNA in  
conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- 20 (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a  
nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:117, and  
extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID  
NO:117 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:117, but  
25 excluding the poly(A) tail at the 3' end of SEQ ID NO:117. Also preferably the  
polynucleotide isolated according to the above process comprises a nucleotide sequence  
corresponding to the cDNA sequence of SEQ ID NO:117 from nucleotide 40 to nucleotide  
207, and extending contiguously from a nucleotide sequence corresponding to the 5' end  
of said sequence of SEQ ID NO:117 from nucleotide 40 to nucleotide 207, to a nucleotide  
30 sequence corresponding to the 3' end of said sequence of SEQ ID NO:117 from nucleotide  
40 to nucleotide 207. Also preferably the polynucleotide isolated according to the above  
process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID

NO:117 from nucleotide 103 to nucleotide 207, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:117 from nucleotide 103 to nucleotide 207, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:117 from nucleotide 103 to nucleotide 207.

5 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:118;
- (b) a fragment of the amino acid sequence of SEQ ID NO:118, the
- 10 fragment comprising eight contiguous amino acids of SEQ ID NO:118; and
- (c) the amino acid sequence encoded by the cDNA insert of clone  
vq26\_1 deposited with the ATCC under accession number PTA-1075;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:118. In further preferred

15 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:118 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:118, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:118 having biological activity, the fragment comprising the amino acid sequence

20 from amino acid 23 to amino acid 32 of SEQ ID NO:118.

In certain preferred embodiments, the polynucleotide is operably linked to an expression control sequence. The invention also provides a host cell, including bacterial, yeast, insect and mammalian cells, transformed with such polynucleotide compositions.

25 Also provided by the present invention are organisms that have enhanced, reduced, or modified expression of the gene(s) corresponding to the polynucleotide sequences disclosed herein.

Processes are also provided for producing a protein, which comprise:

- (a) growing a culture of the host cell transformed with such
- 30 polynucleotide compositions in a suitable culture medium; and
- (b) purifying the protein from the culture.

The protein produced according to such methods is also provided by the present invention.



Protein compositions of the present invention may further comprise a pharmaceutically acceptable carrier. Compositions comprising an antibody which specifically reacts with such protein are also provided by the present invention.

Methods are also provided for preventing, treating or ameliorating a medical condition which comprises administering to a mammalian subject a therapeutically effective amount of a composition comprising a protein of the present invention and a pharmaceutically acceptable carrier.

### BRIEF DESCRIPTION OF THE DRAWINGS

Figures 1A and 1B are schematic representations of the pED6 and pNOTs vectors, respectively, used for deposit of clones disclosed herein.

### DETAILED DESCRIPTION

#### ISOLATED PROTEINS AND POLYNUCLEOTIDES

Nucleotide and amino acid sequences, as presently determined, are reported below for each clone and protein disclosed in the present application. The nucleotide sequence of each clone can readily be determined by sequencing of the deposited clone in accordance with known methods. The predicted amino acid sequence (both full-length and mature forms) can then be determined from such nucleotide sequence. The amino acid sequence of the protein encoded by a particular clone can also be determined by expression of the clone in a suitable host cell, collecting the protein and determining its sequence. For each disclosed protein applicants have identified what they have determined to be the reading frame best identifiable with sequence information available at the time of filing.

As used herein a "secreted" protein is one which, when expressed in a suitable host cell, is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence. "Secreted" proteins include without limitation proteins secreted wholly (e.g., soluble proteins) or partially (e.g., receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins which are transported across the membrane of the endoplasmic reticulum.

Clone "vc62\_1"

A polynucleotide of the present invention has been identified as clone "vc62\_1". vc62\_1 was isolated from a human fetal brain cDNA library and was identified as  
5 encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vc62\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vc62\_1 protein").

The nucleotide sequence of vc62\_1 as presently determined is reported in SEQ ID NO:1, and includes a poly(A) tail. What applicants presently believe to be the proper  
10 reading frame and the predicted amino acid sequence of the vc62\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:2. Amino acids 3 to 15 of SEQ ID NO:2 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 16. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted  
15 leader/signal sequence not be separated from the remainder of the vc62\_1 protein. If the 'G' residue at position 254 of SEQ ID NO:1 were deleted, another potential vc62\_1 reading frame and predicted amino acid sequence that would then be encoded by nucleotides 27 to 365 of SEQ ID NO:1 is reported in SEQ ID NO:169.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone  
20 vc62\_1 should be approximately 4221 bp.

The nucleotide sequence disclosed herein for vc62\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vc62\_1 demonstrated at least some similarity with sequences identified as AA580489 (nn22a10.s1 NCI\_CGAP\_Co12 Homo sapiens cDNA clone  
25 IMAGE 1084602, mRNA sequence), AF047042 (Homo sapiens citrate synthase mRNA, complete cds), and T04200 (Sugar beet citrate synthase cDNA; standard; cDNA to mRNA). The predicted amino acid sequence disclosed herein for vc62\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vc62\_1 protein demonstrated at least some similarity to  
30 sequences identified as AF047042 (citrate synthase [Homo sapiens]) and R82839 (Sugar beet citrate synthase). Based upon sequence similarity, vc62\_1 proteins and each similar protein or peptide may share at least some activity.

Clone "vp10\_1"

A polynucleotide of the present invention has been identified as clone "vp10\_1". vp10\_1 was isolated from a human adult prostate cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vp10\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vp10\_1 protein").

The nucleotide sequence of vp10\_1 as presently determined is reported in SEQ ID NO:3, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vp10\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:4. Amino acids 19 to 31 of SEQ ID NO:4 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 32. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vp10\_1 protein. If another 'G' residue were inserted in SEQ ID NO:3 after the 'G' residue at position 868, another potential vp10\_1 reading frame and predicted amino acid sequence that would be encoded by what would then be nucleotides 6 to 968 of SEQ ID NO:3 is reported in SEQ ID NO:170.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vp10\_1 should be approximately 1401 bp.

The nucleotide sequence disclosed herein for vp10\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vp10\_1 demonstrated at least some similarity with sequences identified as AA733074 (zg79d07.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 399565 3' similar to WP:C15H9.5 CE06834; mRNA sequence). The predicted amino acid sequence disclosed herein for vp10\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vp10\_1 protein demonstrated at least some similarity to the sequence identified as U56965 (unknown protein [Caenorhabditis elegans]). Based upon sequence similarity, vp10\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the vp10\_1 protein sequence centered around amino acid 270 of SEQ ID NO:4.

Clone "vp11\_1"

A polynucleotide of the present invention has been identified as clone "vp11\_1". vp11\_1 was isolated from a human adult prostate cDNA library and was identified as  
5 encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vp11\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vp11\_1 protein").

The nucleotide sequence of vp11\_1 as presently determined is reported in SEQ ID NO:5, and includes a poly(A) tail. What applicants presently believe to be the proper  
10 reading frame and the predicted amino acid sequence of the vp11\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:6. Amino acids 5 to 17 of SEQ ID NO:6 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 18. Due to the hydrophobic nature of the predicted  
15 leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vp11\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vp11\_1 should be approximately 1329 bp.

The nucleotide sequence disclosed herein for vp11\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and  
20 FASTA search protocols. No hits were found in the database.

Clone "vp13\_1"

A polynucleotide of the present invention has been identified as clone "vp13\_1". vp13\_1 was isolated from a human adult prostate cDNA library and was identified as  
25 encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vp13\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vp13\_1 protein").

The nucleotide sequence of vp13\_1 as presently determined is reported in SEQ ID NO:7, and includes a poly(A) tail. What applicants presently believe to be the proper  
30 reading frame and the predicted amino acid sequence of the vp13\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:8. Amino acids 13 to 25 of SEQ ID NO:8 are a predicted leader/signal sequence, with the predicted mature amino

acid sequence beginning at amino acid 26. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vp13\_1 protein.

Other potential vp13\_1 reading frames and predicted amino acid sequences are encoded by nucleotides 151 to 267 of SEQ ID NO:7, with the encoded amino acid sequence reported in SEQ ID NO:171, and by nucleotides 209 to 787 of SEQ ID NO:7, with the encoded amino acid sequence reported in SEQ ID NO:172. Amino acids 1 to 13 of SEQ ID NO:172 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 14. Due to the hydrophobic nature of this predicted leader/signal sequence, it is likely to act as a transmembrane domain should it not be separated from the remainder of the protein of SEQ ID NO:172. The protein of SEQ ID NO:172 also demonstrates significant homology to the human Notch protein, Delta proteins from various species, and other EGF-repeat-containing transmembrane proteins. A deletion or insertion causing a frame-shift in the nucleotide sequence of SEQ ID NO:7 in the region approximately between nucleotides 208 and 267 of SEQ ID NO:7 could join the reading frames of SEQ ID NO:171 and SEQ ID NO:172 into a single reading frame encoding an EGF-repeat-containing protein. Further, the region approximately between nucleotides 605 and 850 may be an alternatively spliced exon.

If the 'A' residue at position 423 of SEQ ID NO:7 were deleted, another potential vp13\_1 reading frame and predicted amino acid sequence that would be encoded by what would then be nucleotides 288 to 503 of SEQ ID NO:7 is reported in SEQ ID NO:173.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vp13\_1 should be approximately 1048 bp.

The nucleotide sequence disclosed herein for vp13\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vp13\_1 demonstrated at least some similarity with sequences identified as AA190865 (zp85b02.s1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone 626955 3' similar to TR G1336628 G1336628 EGF REPEAT TRANSMEMBRANE PROTEIN; mRNA sequence), and U57368 (Mus musculus EGF repeat transmembrane protein mRNA, complete cds). The predicted amino acid sequence disclosed herein for vp13\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vp13\_1 protein demonstrated at least

some similarity to sequences identified as AC004663 (Notch 3 [Homo sapiens]), R28960 (Delta D11), and U57368 (EGF repeat transmembrane protein [Mus musculus]). Based upon sequence similarity, vp13\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential  
5 transmembrane domain within the vp13\_1 protein sequence centered around amino acid 56 of SEQ ID NO:8.

#### Clone "vp16\_1"

A polynucleotide of the present invention has been identified as clone "vp16\_1".  
10 vp16\_1 was isolated from a human adult prostate cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vp16\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vp16\_1 protein").

The nucleotide sequence of vp16\_1 as presently determined is reported in SEQ ID  
15 NO:9, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vp16\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:10. Amino acids 34 to 46 of SEQ ID NO:10 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 47. Due to the hydrophobic nature of the predicted  
20 leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vp16\_1 protein. Another potential vp16\_1 reading frame and predicted amino acid sequence is encoded by basepairs 1621 to 1839 of SEQ ID NO:9 and is reported in SEQ ID NO:174.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone  
25 vp16\_1 should be approximately 2105 bp.

The nucleotide sequence disclosed herein for vp16\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vp16\_1 demonstrated at least some similarity with sequences identified as AA523851 (ng31e01.s1 NCI\_CGAP\_Co3 Homo sapiens cDNA clone  
30 IMAGE:936408, mRNA sequence). Based upon sequence similarity, vp16\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two potential transmembrane domains within the vp16\_1 protein

sequence, one centered around amino acid 36 and another around amino acid 69 of SEQ ID NO:10. The nucleotide sequence of vp16\_1 indicates that it may contain an Alu repetitive element.

5        Clone "vp21\_1"

A polynucleotide of the present invention has been identified as clone "vp21\_1". vp21\_1 was isolated from a human adult prostate cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vp21\_1 is a full-length clone, including the  
10    entire coding sequence of a secreted protein (also referred to herein as "vp21\_1 protein").

The nucleotide sequence of vp21\_1 as presently determined is reported in SEQ ID NO:11, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vp21\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:12. Amino acids 62 to 74  
15    of SEQ ID NO:12 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 75. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vp21\_1 protein. Another potential vp21\_1 reading frame and predicted amino acid sequence encoded by  
20    basepairs 598 to 831 of SEQ ID NO:11 is reported in SEQ ID NO:175. Amino acids 1 to 6 of SEQ ID NO:175 and amino acids 41 to 43 of SEQ ID NO:175 are predicted leader/signal sequences, with the predicted mature amino acid sequences beginning at amino acid 7 or at amino acid 44, respectively.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone  
25    vp21\_1 should be approximately 1538 bp.

The nucleotide sequence disclosed herein for vp21\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vp21\_1 demonstrated at least some similarity with sequences identified as AC004076 (Homo sapiens chromosome 19, cosmid R30217, complete  
30    sequence). The predicted amino acid sequence disclosed herein for vp21\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vp21\_1 protein demonstrated at least some similarity to

sequences identified as AC003682 (Zinc finger protein F18547\_1 [Homo sapiens]) and W19106 (Tat pheromone receptor VN5). Based upon sequence similarity, vp21\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts potential transmembrane domains within the predicted vp21\_1 protein sequences, one centered around amino acid 70 of SEQ ID NO:12, and one centered around amino acid 17 of SEQ ID NO:175.

#### Clone "vp22\_1"

A polynucleotide of the present invention has been identified as clone "vp22\_1". vp22\_1 was isolated from a human adult prostate cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vp22\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vp22\_1 protein").

The nucleotide sequence of vp22\_1 as presently determined is reported in SEQ ID NO:13, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vp22\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:14. Amino acids 13 to 25 of SEQ ID NO:14 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 26. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vp22\_1 protein. Another potential vp22\_1 reading frame and predicted amino acid sequence encoded by basepairs 408 to 1154 of SEQ ID NO:13 is reported in SEQ ID NO:176. Amino acids 40 to 52 of SEQ ID NO:176 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 53. Due to the hydrophobic nature of this predicted leader/signal sequence, it is likely to act as a transmembrane domain should it not be separated from the remainder of the protein of SEQ ID NO:176. A frameshift within the nucleotide sequence of SEQ ID NO:13 approximately between nucleotides 163 and 477 could join the openreading frames of SEQ ID NO:14 and SEQ ID NO:176.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vp22\_1 should be approximately 1718 bp.



The nucleotide sequence disclosed herein for vp22\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vp22\_1 demonstrated at least some similarity with sequences identified as AA526186 (ni94h03.s1 NCI\_CGAP\_Pr21 Homo sapiens cDNA clone  
5 IMAGE:984533, mRNA sequence), AA570505 (nk64h01.s1 NCI\_CGAP\_Sch1 Homo sapiens cDNA clone IMAGE 1018321, mRNA sequence), AB006085 (Danio rerio mRNA for MINDIN2, complete cds), and T78360 (Human neuronal attachment factor-1 DNA; standard; DNA). The predicted amino acid sequence disclosed herein for vp22\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the  
10 BLASTX search protocol. The predicted vp22\_1 protein demonstrated at least some similarity to sequences identified as AB006085 (MINDIN2 [Danio rerio]) and W23663 (Human neuronal attachment factor-1). Based upon sequence similarity, vp22\_1 proteins and each similar protein or peptide may share at least some activity.

15        Clone "vq2\_1"

A polynucleotide of the present invention has been identified as clone "vq2\_1". vq2\_1 was isolated from a human adult lung cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vq2\_1 is a full-length clone, including the entire coding  
20 sequence of a secreted protein (also referred to herein as "vq2\_1 protein").

The nucleotide sequence of vq2\_1 as presently determined is reported in SEQ ID NO:15, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vq2\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:16. Amino acids 4 to 16  
25 of SEQ ID NO:16 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 17. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vq2\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone  
30 vq2\_1 should be approximately 896 bp.

The nucleotide sequence disclosed herein for vq2\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and

FASTA search protocols. vq2\_1 demonstrated at least some similarity with sequences identified as AI203981 (qe76h05.x1 Soares\_fetal\_lung\_NbHL19W Homo sapiens cDNA clone IMAGE:1744953 3', mRNA sequence) and T97082 (Human haematopoietic-specific protein (HSP) DNA; standard; DNA). The predicted amino acid sequence disclosed herein  
5 for vq2\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vq2\_1 protein demonstrated at least some similarity to the sequence identified as W35904 (Human haematopoietic-specific protein (HSP)). Based upon sequence similarity, vq2\_1 proteins and each similar protein or peptide may share at least some activity.

10

Clone "vq3\_1"

A polynucleotide of the present invention has been identified as clone "vq3\_1". vq3\_1 was isolated from a human adult lung cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid  
15 sequence of the encoded protein. vq3\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vq3\_1 protein").

The nucleotide sequence of vq3\_1 as presently determined is reported in SEQ ID NO:17, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vq3\_1 protein corresponding  
20 to the foregoing nucleotide sequence is reported in SEQ ID NO:18. Amino acids 11 to 23 of SEQ ID NO:18 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 24. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vq3\_1 protein.

25 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vq3\_1 should be approximately 1490 bp.

The nucleotide sequence disclosed herein for vq3\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No significant hits were found in the database. The nucleotide  
30 sequence of vq3\_1 indicates that it may contain an Alu repetitive element.

Clone "vq5\_1"

A polynucleotide of the present invention has been identified as clone "vq5\_1". vq5\_1 was isolated from a human adult lung cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid  
5 sequence of the encoded protein. vq5\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vq5\_1 protein").

The nucleotide sequence of vq5\_1 as presently determined is reported in SEQ ID NO:19, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vq5\_1 protein corresponding  
10 to the foregoing nucleotide sequence is reported in SEQ ID NO:20. Amino acids 9 to 21 of SEQ ID NO:20 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 22. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vq5\_1 protein.

15 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vq5\_1 should be approximately 2207 bp.

The nucleotide sequence disclosed herein for vq5\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vq5\_1 demonstrated at least some similarity with sequences  
20 identified as AQ036276 (CIT-HSP-2331M15.TF CIT-HSP Homo sapiens genomic clone 2331M15, genomic survey sequence) and T24918 (Human gene signature HUMGS07027; standard; cDNA to mRNAP). Based upon sequence similarity, vq5\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts that the signal sequence at residue 22 of SEQ ID NO:20 is also a  
25 potential transmembrane domain.

Clone "vq6\_1"

A polynucleotide of the present invention has been identified as clone "vq6\_1". vq6\_1 was isolated from a human adult lung cDNA library and was identified as encoding  
30 a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vq6\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vq6\_1 protein").

The nucleotide sequence of vq6\_1 as presently determined is reported in SEQ ID NO:21, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vq6\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:22. Amino acids 6 to 18 of SEQ ID NO:22 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 19. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vq6\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vq6\_1 should be approximately 1875 bp.

The nucleotide sequence disclosed herein for vq6\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vq6\_1 demonstrated at least some similarity with sequences identified as AA729043 (nw22d09.s1 NCI\_CGAP\_GCB0 Homo sapiens cDNA clone IMAGE:1241201 similar to contains Alu repetitive element; mRNA sequence). Based upon sequence similarity, vq6\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts an additional potential transmembrane domain within the vq6\_1 protein sequence centered around amino acid 37 of SEQ ID NO:22. The nucleotide sequence of vq6\_1 indicates that it may contain an Alu repetitive element.

#### Clone "vr1\_1"

A polynucleotide of the present invention has been identified as clone "vr1\_1". vr1\_1 was isolated from a human adult muscle cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vr1\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vr1\_1 protein").

The nucleotide sequence of vr1\_1 as presently determined is reported in SEQ ID NO:23, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vr1\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:24. Amino acids 34 to 46 of SEQ ID NO:24 are a predicted leader/signal sequence, with the predicted mature amino

acid sequence beginning at amino acid 47. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vr1\_1 protein. The region of SEQ ID NO:23 approximately between nucleotides 1931 and 1977 of SEQ ID NO:23 may be an alternatively spliced exon.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vr1\_1 should be approximately 1512 bp.

The nucleotide sequence disclosed herein for vr1\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vr1\_1 demonstrated at least some similarity with sequences identified as AL031602 (Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1174N9; HTGS phase 1), I64695 (Sequence 1 from patent US 5665588), and T35233 (Natural killer lytic associated protein cDNA; standard; cDNA). The predicted amino acid sequence disclosed herein for vr1\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vr1\_1 protein demonstrated at least some similarity to sequences identified as R99256 (Natural killer lytic associated protein), and X71642 (GEG-154 gene product [Mus musculus]). Based upon sequence similarity, vr1\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts an additional potential transmembrane domain within the vr1\_1 protein sequence centered around amino acid 150 of SEQ ID NO:24.

#### Clone "vc63\_1"

A polynucleotide of the present invention has been identified as clone "vc63\_1". vc63\_1 was isolated from a human fetal brain cDNA library and was identified as encoding a novel protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vc63\_1 is a full-length clone, including the entire coding sequence of a novel protein (also referred to herein as "vc63\_1 protein").

The nucleotide sequence of vc63\_1 as presently determined is reported in SEQ ID NO:25, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vc63\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:26. Another potential

vc63\_1 reading frame and predicted amino acid sequence encoded by basepairs 528 to 1100 of SEQ ID NO:25 is reported in SEQ ID NO:177. Amino acids 140 to 152 of SEQ ID NO:177 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 153. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein of SEQ ID NO:177.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vc63\_1 should be approximately 2397 bp.

10 The nucleotide sequence disclosed herein for vc63\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vc63\_1 demonstrated at least some similarity with sequences identified as N66555 (yy69b07.s1 Homo sapiens cDNA clone 278773 3') and T21367 (Human gene signature HUMGS02731; standard; cDNA to mRNA). The predicted amino acid sequence disclosed herein for vc63\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vc63\_1 protein demonstrated at least some similarity to the sequence identified as Z36948 (D2089.2 [Caenorhabditis elegans]). Based upon sequence similarity, vc63\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the protein sequence of SEQ ID NO:177, centered around amino acid 153 of SEQ ID NO:177.

#### Clone "vb25\_1"

A polynucleotide of the present invention has been identified as clone "vb25\_1". vb25\_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vb25\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vb25\_1 protein").

The nucleotide sequence of vb25\_1 as presently determined is reported in SEQ ID NO:27, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vb25\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:28. Amino acids 5 to 17

of SEQ ID NO:28 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 18. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vb25\_1 protein.

- 5           The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vb25\_1 should be approximately 1677 bp.

The nucleotide sequence disclosed herein for vb25\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vb25\_1 demonstrated at least some similarity with sequences  
10 identified as Z73429 (Human DNA sequence from cosmid cN32F9 on chromosome 22q11.2-qter Contains CpG island). Based upon sequence similarity, vb25\_1 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of vb25\_1 indicates that it may contain one or more of the following repetitive elements: AC simple repeat, AG simple repeat, ALU, MIR.

15

Clone "vb27\_1"

A polynucleotide of the present invention has been identified as clone "vb27\_1". vb27\_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the  
20 amino acid sequence of the encoded protein. vb27\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vb27\_1 protein").

The nucleotide sequence of vb27\_1 as presently determined is reported in SEQ ID NO:29, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vb27\_1 protein corresponding  
25 to the foregoing nucleotide sequence is reported in SEQ ID NO:30. Amino acids 14 to 26 of SEQ ID NO:30 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 27. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vb27\_1 protein.

- 30           The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vb27\_1 should be approximately 3456 bp.

The nucleotide sequence disclosed herein for vb27\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vb27\_1 demonstrated at least some similarity with sequences identified as AC005035 (Homo sapiens BAC clone NH0353P23 from 2, complete  
5 sequence) and H73579 (yu29f09.r1 Homo sapiens cDNA clone 235241 5'). Based upon sequence similarity, vb27\_1 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of vb27\_1 indicates that it may contain one or more of the following repetitive elements: ALU, Mer3.

10        Clone "vb28\_1"

A polynucleotide of the present invention has been identified as clone "vb28\_1". vb28\_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vb28\_1 is a full-length clone, including the  
15 entire coding sequence of a secreted protein (also referred to herein as "vb28\_1 protein").

The nucleotide sequence of vb28\_1 as presently determined is reported in SEQ ID NO:31, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vb28\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:32. Amino acids 4 to 16  
20 of SEQ ID NO:32 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 17. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vb28\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone  
25 vb28\_1 should be approximately 3008 bp.

The nucleotide sequence disclosed herein for vb28\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vb28\_1 demonstrated at least some similarity with sequences identified as AA046671 (zf12d09.r1 Soares\_fetal\_heart\_NbHH19W Homo sapiens cDNA  
30 clone IMAGE:376721 5' similar to PIR:A38745 A38745 cell adhesion molecule CD44 precursor - rat; mRNA sequence) and V22687 (DNA encoding a CD44-like protein). The predicted amino acid sequence disclosed herein for vb28\_1 was searched against the



GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vb28\_1 protein demonstrated at least some similarity to sequences identified as W56249 (Amino acid sequence of a CD44-like protein) and X66081 (CD44 [Mus musculus]). Based upon sequence similarity, vb28\_1 proteins and each similar protein or  
5 peptide may share at least some activity.

#### Clone "vb29\_1"

A polynucleotide of the present invention has been identified as clone "vb29\_1". vb29\_1 was isolated from a human fetal brain cDNA library and was identified as  
10 encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vb29\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vb29\_1 protein").

The nucleotide sequence of vb29\_1 as presently determined is reported in SEQ ID NO:33, and includes a poly(A) tail. What applicants presently believe to be the proper  
15 reading frame and the predicted amino acid sequence of the vb29\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:34. Amino acids 11 to 23 of SEQ ID NO:34 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 24. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted  
20 leader/signal sequence not be separated from the remainder of the vb29\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vb29\_1 should be approximately 2970 bp.

The nucleotide sequence disclosed herein for vb29\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and  
25 FASTA search protocols. vb29\_1 demonstrated at least some similarity with sequences identified as AA084068 (zn16d12.r1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone 547607 5', mRNA sequence) and AQ418918 (RPCI-11-185K12.TV RPCI-11 Homo sapiens genomic clone RPCI-11-185K12, genomic survey sequence). Based upon sequence similarity, vb29\_1 proteins and each similar  
30 protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the vb29\_1 protein sequence centered

around amino acid 41 of SEQ ID NO:34. The nucleotide sequence of vb29\_1 indicates that it may contain an Alu repetitive element.

Clone "vb30\_1"

5 A polynucleotide of the present invention has been identified as clone "vb30\_1". vb30\_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vb30\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vb30\_1 protein").

10 The nucleotide sequence of vb30\_1 as presently determined is reported in SEQ ID NO:35, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vb30\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:36. Amino acids 15 to 27 of SEQ ID NO:36 are a predicted leader/signal sequence, with the predicted mature amino  
15 acid sequence beginning at amino acid 28. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vb30\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vb30\_1 should be approximately 3325 bp.

20 The nucleotide sequence disclosed herein for vb30\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No significant hits were found in the databases. The nucleotide sequence of vb30\_1 indicates that it may contain an Alu repetitive element.

Clone "vc67\_1"

25 A polynucleotide of the present invention has been identified as clone "vc67\_1". vc67\_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vc67\_1 is a full-length clone, including the  
30 entire coding sequence of a secreted protein (also referred to herein as "vc67\_1 protein").

The nucleotide sequence of vc67\_1 as presently determined is reported in SEQ ID NO:37, and includes a poly(A) tail. What applicants presently believe to be the proper

reading frame and the predicted amino acid sequence of the vc67\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:38. Another potential vc67\_1 reading frame and predicted amino acid sequence encoded by basepairs 3 to 242 of SEQ ID NO:37 is reported in SEQ ID NO:178.

- 5           The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vc67\_1 should be approximately 2305 bp.

          The nucleotide sequence disclosed herein for vc67\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vc67\_1 demonstrated at least some similarity with sequences  
10 identified as T23222 (Human gene signature HUMGS05018), W87297 (zh67h03.s1 Soares\_fetal\_liver\_spleen\_1NFLS\_S1 Homo sapiens cDNA clone IMAGE 417173 3', mRNA sequence), and Z97201 (Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 94M16, WORKING DRAFT SEQUENCE). The predicted amino acid sequence disclosed herein for vc67\_1 was searched against the GenPept and  
15 GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vc67\_1 protein demonstrated at least some similarity to sequences identified as W69427 (Human secreted protein bk291\_3) and Z68751 (Similarity to Yeast hypothetical protein YKK0 (SW YKK0\_YEAST); cDNA EST EMBL C12578 comes from this gene; cDNA EST yk329g12.5 comes from this gene; cDNA EST yk415). Based upon sequence  
20 similarity, vc67\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two potential transmembrane domains within the vc67\_1 protein sequence of SEQ ID NO:38, one centered around amino acid 58 and another around amino acid 85 of SEQ ID NO:38.

25           Clone "vf4\_1"

          A polynucleotide of the present invention has been identified as clone "vf4\_1". vf4\_1 was isolated from a human adult heart cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vf4\_1 is a full-length clone, including the entire coding  
30 sequence of a secreted protein (also referred to herein as "vf4\_1 protein").

          The nucleotide sequence of vf4\_1 as presently determined is reported in SEQ ID NO:39, and includes a poly(A) tail. What applicants presently believe to be the proper

reading frame and the predicted amino acid sequence of the vf4\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:40. Amino acids 5 to 17 of SEQ ID NO:40 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 18. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vf4\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vf4\_1 should be approximately 972 bp.

The nucleotide sequence disclosed herein for vf4\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vf4\_1 demonstrated at least some similarity with sequences identified as AA813690 (ai71a09.s1 Soares\_testis\_NHT Homo sapiens cDNA clone 1376248 3', mRNA sequence) and V86544 (EST clone AZ285). Based upon sequence similarity, vf4\_1 proteins and each similar protein or peptide may share at least some activity.

#### Clone "vg3\_1"

A polynucleotide of the present invention has been identified as clone "vg3\_1". vg3\_1 was isolated from a human adult brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vg3\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vg3\_1 protein").

The nucleotide sequence of vg3\_1 as presently determined is reported in SEQ ID NO:41, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vg3\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:42. Amino acids 13 to 25 of SEQ ID NO:42 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 26. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vg3\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vg3\_1 should be approximately 3667 bp.

The nucleotide sequence disclosed herein for vg3\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vg3\_1 demonstrated at least some similarity with sequences identified as AI283122 (qm51h10.x1 Soares\_placenta\_8to9weeks\_2NbHP8to9W Homo sapiens cDNA clone IMAGE 1892323 3', mRNA sequence). The predicted amino acid sequence disclosed herein for vg3\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vg3\_1 protein demonstrated at least some similarity to sequences identified as U53155 (ZC513.5 [Caenorhabditis elegans]). Based upon sequence similarity, vg3\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts the following transmembrane domains within the vg3\_1 protein sequence: four certain transmembrane domains centered around amino acids 78, 133, 156, and 298 of SEQ ID NO:42, respectively; four strongly putative transmembrane domains centered around amino acids 105, 189, 221, and 354 of SEQ ID NO:42, respectively; and six possible transmembrane domains centered around amino acids 262, 272, 322, 367, 432, and 460 of SEQ ID NO:42, respectively. Motifs analysis detected a Crystallins beta and gamma 'Greek key' motif signature around amino acid 52 of SEQ ID NO:42. The nucleotide sequence of vg3\_1 indicates that it may contain an Alu repetitive element.

#### 20      Clone "vo2\_1"

A polynucleotide of the present invention has been identified as clone "vo2\_1". vo2\_1 was isolated from a human adult pancreas cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo2\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vo2\_1 protein").

The nucleotide sequence of vo2\_1 as presently determined is reported in SEQ ID NO:43, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vo2\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:44.

30      Another potential vo2\_1 reading frame and predicted amino acid sequence encoded by basepairs 95 to 280 of SEQ ID NO:43 is reported in SEQ ID NO:179. Amino acids 9 to 21 of SEQ ID NO:179 are a predicted leader/signal sequence, with the predicted mature

amino acid sequence beginning at amino acid 22. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein of SEQ ID NO:179.

5           Another potential vo2\_1 reading frame and predicted amino acid sequence encoded by basepairs 76 to 258 of SEQ ID NO:43 is reported in SEQ ID NO:180. Amino acids 18 to 30 of SEQ ID NO:180 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 31. Due to the hydrophobic nature of this predicted leader/signal sequence, it is likely to act as a transmembrane domain should it  
10   not be separated from the remainder of the protein of SEQ ID NO:180.

          Another potential vo2\_1 reading frame and predicted amino acid sequence encoded by basepairs 2131 to 2310 of SEQ ID NO:43 is reported in SEQ ID NO:181. Amino acids 38 to 50 of SEQ ID NO:181 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 11; amino acids 19 to 31 of SEQ ID  
15   NO:181 are also a possible leader/signal sequence, with the predicted mature amino acid sequence in this case beginning at amino acid 32. Due to the hydrophobic nature of these predicted leader/signal sequences, each is likely to act as a transmembrane domain should it not be separated from the remainder of the protein of SEQ ID NO:181.

          The EcoRI/NotI restriction fragment obtainable from the deposit containing clone  
20   vo2\_1 should be approximately 2903 bp.

          The nucleotide sequence disclosed herein for vo2\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vo2\_1 demonstrated at least some similarity with sequences identified as AI094627 (oy61b07.s1 NCI\_CGAP\_Brn23 Homo sapiens cDNA clone  
25   IMAGE 1670293 3', mRNA sequence). Based upon sequence similarity, vo2\_1 proteins and each similar protein or peptide may share at least some activity.

#### Clone "vo3\_1"

          A polynucleotide of the present invention has been identified as clone "vo3\_1".  
30   vo3\_1 was isolated from a human adult pancreas cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the

amino acid sequence of the encoded protein. vo3\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vo3\_1 protein").

The nucleotide sequence of vo3\_1 as presently determined is reported in SEQ ID NO:45, and includes a poly(A) tail. What applicants presently believe to be the proper  
5 reading frame and the predicted amino acid sequence of the vo3\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:46. Amino acids 107 to 119 of SEQ ID NO:46 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 120. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the  
10 predicted leader/signal sequence not be separated from the remainder of the vo3\_1 protein.

If a "C" residue were to be deleted from the nucleotide sequence of SEQ ID NO:45 at either position 917 or position 918, another potential vo3\_1 reading frame and predicted amino acid sequence encoded by what would then be basepairs 697 to 1377 of SEQ ID NO:45 is reported in SEQ ID NO:182. Amino acids 62 to 74 of SEQ ID NO:182 are a  
15 predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 75. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein of SEQ ID NO:182.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone  
20 vo3\_1 should be approximately 1592 bp.

The nucleotide sequence disclosed herein for vo3\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vo3\_1 demonstrated at least some similarity with sequences identified as AA530997 (nj07a06.s1 NCI\_CGAP\_Pr22 Homo sapiens cDNA clone  
25 IMAGE:985618 3', mRNA sequence), AA683481 (zl55b03.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone IMAGE:505805 3', mRNA sequence), D88158 (Pig mRNA for cytochrome b561, complete cds), and V84516 (Human secreted protein gene 106 clone HTOEY16). The predicted amino acid sequence disclosed herein for vo3\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the  
30 BLASTX search protocol. The predicted vo3\_1 protein demonstrated at least some similarity to sequences identified as U06715 (HCYTO B561 [Homo sapiens]) and W89024 (Polypeptide fragment encoded by gene 156). Based upon sequence similarity, vo3\_1

proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts five potential transmembrane domains within the vo3\_1 protein sequence, centered around amino acids 35, 75, 113, 146, and 191 of SEQ ID NO:46, respectively.

5

Clone "vo5\_1"

A polynucleotide of the present invention has been identified as clone "vo5\_1". vo5\_1 was isolated from a human adult pancreas cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo5\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vo5\_1 protein").

The nucleotide sequence of vo5\_1 as presently determined is reported in SEQ ID NO:47, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vo5\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:48. Amino acids 8 to 20 of SEQ ID NO:48 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 21. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vo5\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vo5\_1 should be approximately 2487 bp.

The nucleotide sequence disclosed herein for vo5\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vo5\_1 demonstrated at least some similarity with sequences identified as AA868551 (ak43f09.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1408745 3', mRNA sequence) and AC005500 (complete sequence [Homo sapiens Chromosome 22q11 PAC Clone p52f6 In DGCR Region]). Based upon sequence similarity, vo5\_1 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of vo5\_1 indicates that it may contain an Alu repetitive element.



Clone "vo6\_1"

A polynucleotide of the present invention has been identified as clone "vo6\_1". vo6\_1 was isolated from a human adult pancreas cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo6\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vo6\_1 protein").

The nucleotide sequence of vo6\_1 as presently determined is reported in SEQ ID NO:49, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vo6\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:50. Amino acids 77 to 89 of SEQ ID NO:50 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 90. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vo6\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vo6\_1 should be approximately 1272 bp.

The nucleotide sequence disclosed herein for vo6\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vo6\_1 demonstrated at least some similarity with sequences identified as AL020989 (Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 192P9; HTGS phase 1), T34592 (NTII-11 nerve protein coding sequence), and U13617 (*Rattus norvegicus* Sprague-Dawley plasmolipin mRNA, complete cds). The predicted amino acid sequence disclosed herein for vo6\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vo6\_1 protein demonstrated at least some similarity to sequences identified as R99799 (NTII-11 nerve protein, facilitates regeneration of nerve cells) and U13617 (plasmolipin [*Rattus norvegicus*]). Plasmolipin is an 18-kDa proteolipid protein found in kidney and brain, where it is restricted to the apical surface of tubular epithelial cells and to mammalian myelinated tracts, respectively; addition of plasmolipin to lipid bilayers induces the formation of ion channels, which are voltage-dependent and K(+)-selective. (See Fischer and Sapirstein, 1994, *J. Biol. Chem.* 269(40): 24912-24919, which is incorporated by reference herein). Based upon sequence similarity, vo6\_1 proteins and

each similar protein or peptide may share at least some activity. The TopPredII computer program predicts three potential transmembrane domains within the vo6\_1 protein sequence, centered around amino acids 14, 42, and 90 of SEQ ID NO:50, respectively.

5           Clone "vo9\_1"

A polynucleotide of the present invention has been identified as clone "vo9\_1". vo9\_1 was isolated from a human adult pancreas cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo9\_1 is a full-length clone, including the  
10   entire coding sequence of a secreted protein (also referred to herein as "vo9\_1 protein").

The nucleotide sequence of vo9\_1 as presently determined is reported in SEQ ID NO:51, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vo9\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:52. Amino acids 22 to 34  
15   of SEQ ID NO: are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 35. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vo9\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone  
20   vo9\_1 should be approximately 3331 bp.

The nucleotide sequence disclosed herein for vo9\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vo9\_1 demonstrated at least some similarity with sequences identified as AA936961 (oo65f04.s1 NCI\_CGAP\_GC4 Homo sapiens cDNA clone  
25   IMAGE 1571071 3', mRNA sequence), AF010496 9Rhodobacter capsulatus strain SB1003, partial genome), AL035661 (Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 568C11, WORKING DRAFT SEQUENCE), and Q24673 (facA gene). The predicted amino acid sequence disclosed herein for vo9\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX  
30   search protocol. The predicted vo9\_1 protein demonstrated at least some similarity to sequences identified as R23968 (facA gene product) and Y15417 (acetate--CoA ligase

[Coprinus cinereus]). Based upon sequence similarity, vo9\_1 proteins and each similar protein or peptide may share at least some activity.

Clone "vo11\_1"

5 A polynucleotide of the present invention has been identified as clone "vo11\_1". vo11\_1 was isolated from a human adult pancreas cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo11\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vo11\_1 protein").

10 The nucleotide sequence of vo11\_1 as presently determined is reported in SEQ ID NO:53, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vo11\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:54. Amino acids 52 to 64 of SEQ ID NO:54 are a predicted leader/signal sequence, with the predicted mature amino

15 acid sequence beginning at amino acid 65.

Another potential vo11\_1 reading frame and predicted amino acid sequence, encoded by basepairs 18 to 308 of SEQ ID NO:53, is reported in SEQ ID NO:183. Amino acids 10 to 22 of SEQ ID NO:183 are a possible leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 23. Due to the hydrophobic nature

20 of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein of SEQ ID NO:183.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vo11\_1 should be approximately 1509 bp.

25 The nucleotide sequence disclosed herein for vo11\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vo11\_1 demonstrated at least some similarity with sequences identified as D83866 (similar to none, mRNA sequence). Based upon sequence similarity, vo11\_1 proteins and each similar protein or peptide may share at least some activity.

30

Clone "vo12\_1"

A polynucleotide of the present invention has been identified as clone "vo12\_1". vo12\_1 was isolated from a human adult pancreas cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo12\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vo12\_1 protein").

The nucleotide sequence of vo12\_1 as presently determined is reported in SEQ ID NO:55, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vo12\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:56. Amino acids 4 to 16 of SEQ ID NO:56 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 17.

Another potential vo12\_1 reading frame and predicted amino acid sequence, encoded by basepairs 107 to 310 of SEQ ID NO:55, is reported in SEQ ID NO:184. Amino acids 14 to 26 and amino acids 18 to 30 of SEQ ID NO:184 are predicted leader/signal sequences, with the predicted mature amino acid sequence beginning at amino acid 27 or at amino acid 31, respectively. Due to the hydrophobic nature of these predicted leader/signal sequences, each is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein of SEQ ID NO:184.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vo12\_1 should be approximately 986 bp.

The nucleotide sequence disclosed herein for vo12\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vo12\_1 demonstrated at least some similarity with sequences identified as AA444152 (zv51g06.r1 Soares testis NHT Homo sapiens cDNA clone 757210 5', mRNA sequence). Based upon sequence similarity, vo12\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the vo12\_1 protein sequence centered around amino acid 51 of SEQ ID NO:56.

Clone "vo13\_1"

A polynucleotide of the present invention has been identified as clone "vo13\_1". vo13\_1 was isolated from a human adult pancreas cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. The vo13\_1 clone includes coding sequence of a secreted protein (also referred to herein as "vo13\_1 protein").

The nucleotide sequence of vo13\_1 as presently determined is reported in SEQ ID NO:57, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vo13\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:58. Amino acids 8 to 20 of SEQ ID NO:58 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 21.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vo13\_1 should be approximately 1073 bp.

The nucleotide sequence disclosed herein for vo13\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vo13\_1 demonstrated at least some similarity with sequences identified as AA988298 (os32a02.s1 NCI\_CGAP\_Br2 Homo sapiens cDNA clone IMAGE:16070183', mRNA sequence) and V69614 (Human secreted protein gene 4 clone HE8ND56). The predicted amino acid sequence disclosed herein for vo13\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vo13\_1 protein demonstrated at least some similarity to sequences identified as W83934 (Human secreted protein from gene 4 clone HE8ND56). Based upon sequence similarity, vo13\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the vo13\_1 protein sequence centered around amino acid 50 of SEQ ID NO:58.

Clone "vo14\_1"

A polynucleotide of the present invention has been identified as clone "vo14\_1". vo14\_1 was isolated from a human adult pancreas cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the

amino acid sequence of the encoded protein. vo14\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vo14\_1 protein").

The nucleotide sequence of vo14\_1 as presently determined is reported in SEQ ID NO:59, and includes a poly(A) tail. What applicants presently believe to be the proper  
5 reading frame and the predicted amino acid sequence of the vo14\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:60. Amino acids 14 to 26 of SEQ ID NO:60 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 27.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone  
10 vo14\_1 should be approximately 1605 bp.

The nucleotide sequence disclosed herein for vo14\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No significant hits were found in the databases. Based upon sequence similarity, vo14\_1 proteins and each similar protein or peptide may share at least  
15 some activity. The nucleotide sequence of vo14\_1 indicates that it may contain one or more of the following repetitive elements: Alu, TAAAA repeat.

#### Clone "vo15\_1"

A polynucleotide of the present invention has been identified as clone "vo15\_1".  
20 vo15\_1 was isolated from a human adult pancreas cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo15\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vo15\_1 protein").

The nucleotide sequence of vo15\_1 as presently determined is reported in SEQ ID  
25 NO:61, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vo15\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:62. Amino acids 13 to 25 of SEQ ID NO:62 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 26.

30 If a nucleotide were deleted between nucleotide 458 and nucleotide 460 of SEQ ID NO:61, another potential vo15\_1 reading frame and predicted amino acid sequence, encoded by what would then be basepairs 90 to 515 of SEQ ID NO:61, is reported in SEQ

ID NO:185. Amino acids 16 to 28 and amino acids 13 to 25 of SEQ ID NO:185 are predicted leader/signal sequences, with the predicted mature amino acid sequence beginning at amino acid 29 or at amino acid 26, respectively. Due to the hydrophobic nature of these predicted leader/signal sequences, each is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein of SEQ ID NO:185.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vo15\_1 should be approximately 2842 bp.

The nucleotide sequence disclosed herein for vo15\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vo15\_1 demonstrated at least some similarity with sequences identified as AI096756 (qb46e10.x1 NCI\_CGAP\_Brn23 Homo sapiens cDNA clone IMAGE 1703178 3', mRNA sequence). Based upon sequence similarity, vo15\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the vo15\_1 protein sequence centered around amino acid 126 of SEQ ID NO:62. The nucleotide sequence of vo15\_1 indicates that it may contain one or more repeat sequences.

#### Clone "vo16\_1"

A polynucleotide of the present invention has been identified as clone "vo16\_1". vo16\_1 was isolated from a human adult pancreas cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo16\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vo16\_1 protein").

The nucleotide sequence of vo16\_1 as presently determined is reported in SEQ ID NO:63, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vo16\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:64. Amino acids 51 to 63 of SEQ ID NO:64 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 64. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vo16\_1 protein.

If an "A" or "G" nucleotide were inserted between nucleotides 102 and 103 of SEQ ID NO:63 and an additional "A" residue inserted between nucleotides 271 and 273 of SEQ ID NO:63, another potential vo16\_1 reading frame and predicted amino acid sequence, encoded by what would then be basepairs 6 to 338 of SEQ ID NO:63, is reported in SEQ ID NO:186. Amino acids 5 to 17 and amino acids 4 to 16 of SEQ ID NO:186 are predicted leader/signal sequences, with the predicted mature amino acid sequence beginning at amino acid 18 or at amino acid 17, respectively. Due to the hydrophobic nature of these predicted leader/signal sequences, each is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein of SEQ ID NO:186.

Another potential vo16\_1 reading frame and predicted amino acid sequence, encoded by basepairs 846 to 1061 of SEQ ID NO:63, is reported in SEQ ID NO:187. Amino acids 12 to 24 and amino acids 11 to 23 of SEQ ID NO:187 are predicted leader/signal sequences, with the predicted mature amino acid sequence beginning at amino acid 25 or at amino acid 24, respectively. Due to the hydrophobic nature of these predicted leader/signal sequences, each is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein of SEQ ID NO:187.

Nucleotides 1 to 133 of SEQ ID NO:63 are nearly identical to nucleotides 862 to 994 of SEQ ID NO:63, resulting in amino acids 1 to 33 of SEQ ID NO:186 being identical to amino acids 8 to 40 of SEQ ID NO:187.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vo16\_1 should be approximately 2113 bp.

The nucleotide sequence disclosed herein for vo16\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vo16\_1 demonstrated at least some similarity with sequences identified as R79825 (yi89a06.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:146386 3', mRNA sequence). Based upon sequence similarity, vo16\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the vo16\_1 protein sequence centered around amino acid 64 of SEQ ID NO:64. The nucleotide sequence of vo16\_1 indicates that it may contain an Alu repeat region.



Clone "vo18\_1"

A polynucleotide of the present invention has been identified as clone "vo18\_1". vo18\_1 was isolated from a human adult pancreas cDNA library and was identified as  
5 encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo18\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vo18\_1 protein").

The nucleotide sequence of vo18\_1 as presently determined is reported in SEQ ID NO:65, and includes a poly(A) tail. What applicants presently believe to be the proper  
10 reading frame and the predicted amino acid sequence of the vo18\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:66. Amino acids 10 to 22 of SEQ ID NO:66 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 23.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone  
15 vo18\_1 should be approximately 624 bp.

The nucleotide sequence disclosed herein for vo18\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vo18\_1 demonstrated at least some similarity with sequences  
20 identified as AI198956 (qf66h01.x1 Soares\_testis\_NHT Homo sapiens cDNA clone IMAGE 1755025 3', mRNA sequence). Based upon sequence similarity, vo18\_1 proteins and each similar protein or peptide may share at least some activity.

Clone "vo19\_1"

A polynucleotide of the present invention has been identified as clone "vo19\_1".  
25 vo19\_1 was isolated from a human adult pancreas cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo19\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vo19\_1 protein").

The nucleotide sequence of vo19\_1 as presently determined is reported in SEQ ID  
30 NO:67, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vo19\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:68. Amino acids 8 to 20

of SEQ ID NO:68 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 21.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vo19\_1 should be approximately 1957 bp.

5       The nucleotide sequence disclosed herein for vo19\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vo19\_1 demonstrated at least some similarity with sequences identified as AI524085 (th01e09.x1 NCI\_CGAP\_CLL1 Homo sapiens cDNA clone IMAGE:2117032 3', mRNA sequence) and V42646 (DNA encoding a human pathogenesis-related protein designated HPRP). The predicted amino acid sequence disclosed herein for vo19\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vo19\_1 protein demonstrated at least some similarity to sequences identified as U16307 (glioma pathogenesis-related protein [Homo sapiens]) and W63115 (A human pathogenesis-related protein designated HPRP). Based upon sequence similarity, vo19\_1 proteins and each similar protein or peptide may share at least some activity.

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#### Clone "vo22\_1"

A polynucleotide of the present invention has been identified as clone "vo22\_1". vo22\_1 was isolated from a human adult pancreas cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo22\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vo22\_1 protein").

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The nucleotide sequence of vo22\_1 as presently determined is reported in SEQ ID NO:69, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vo22\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:70. Amino acids 6 to 18 of SEQ ID NO:70 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 19.

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30       If one of the "G" nucleotides at positions 385 and 386 of SEQ ID NO:69 were deleted, and the "G" residue at position 312 of SEQ ID NO:69 changed to a "T", another potential vo22\_1 reading frame and predicted amino acid sequence, encoded by what

would then be basepairs 104 to 430 of SEQ ID NO:69, is reported in SEQ ID NO:188. Amino acids 8 to 20, amino acids 7 to 19, amino acids 6 to 18, and amino acids 9 to 21 of SEQ ID NO:188 are predicted leader/signal sequences, with the predicted mature amino acid sequence beginning at amino acid 21, or at amino acid 20, or at amino acid 19, or at amino acid 22, respectively. Due to the hydrophobic nature of these predicted leader/signal sequences, each is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein of SEQ ID NO:188.

Another potential vo22\_1 reading frame and predicted amino acid sequence, encoded by basepairs 1150 to 1357 of SEQ ID NO:69, is reported in SEQ ID NO:189. Amino acids 3 to 15 of SEQ ID NO:189 are a possible leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 16. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein of SEQ ID NO:189.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vo22\_1 should be approximately 2091 bp.

The nucleotide sequence disclosed herein for vo22\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vo22\_1 demonstrated at least some similarity with sequences identified as AA706247 (ah28c11.s1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone 1240148 3', mRNA sequence) and V34194 (Human secreted protein gene 41 clone HNTME13). The predicted amino acid sequence disclosed herein for vo22\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vo22\_1 protein demonstrated at least some similarity to sequences identified as AF01644 (No definition line found [Caenorhabditis elegans]) and W75155 (Human secreted protein encoded by gene 41 clone HNTME13). Based upon sequence similarity, vo22\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts 9 potential transmembrane domains within the vo22\_1 protein sequence, centered around amino acids 50, 120, 165, 250, 275, 309, 356, 374, and 392 of SEQ ID NO:70, respectively.

Clone "vo23\_1"

A polynucleotide of the present invention has been identified as clone "vo23\_1". vo23\_1 was isolated from a human adult pancreas cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo23\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vo23\_1 protein").

The nucleotide sequence of vo23\_1 as presently determined is reported in SEQ ID NO:71, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vo23\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:72.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vo23\_1 should be approximately 2598 bp.

The nucleotide sequence disclosed herein for vo23\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vo23\_1 demonstrated at least some similarity with sequences identified as T23658 (Human gene signature HUMGS05523), W81246 (zd85b01.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 347401 5', mRNA sequence), and Z84488 (Human DNA sequence from PAC 93H18 on chromosome 6 contains ESTs heterochromatin protein HP1Hs-gamma pseudogene, STS and CpG island). Based upon sequence similarity, vo23\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two potential transmembrane domains within the vo23\_1 protein sequence, one centered around amino acid 428 and another around amino acid 472 of SEQ ID NO:72.

Clone "vo24\_1"

A polynucleotide of the present invention has been identified as clone "vo24\_1". vo24\_1 was isolated from a human adult pancreas cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo24\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vo24\_1 protein").

The nucleotide sequence of vo24\_1 as presently determined is reported in SEQ ID NO:73, and includes a poly(A) tail. What applicants presently believe to be the proper

reading frame and the predicted amino acid sequence of the vo24\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:74. Amino acids 10 to 22 of SEQ ID NO:74 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 23.

- 5           The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vo24\_1 should be approximately 3484 bp.

          The nucleotide sequence disclosed herein for vo24\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vo24\_1 demonstrated at least some similarity with sequences  
10 identified as AC003117 (\*\*\*) SEQUENCING IN PROGRESS (\*\*\*) Human chromosome 1 BAC 308G1 genomic sequence; HTGS phase 1, 3 unordered pieces), V10696 (Human 3.5 kB DNA fragment predicted to contain CH1-9a11-2 gene), and Z94054 (Human DNA sequence from PAC 125H23 on chromosome 1q24-1q25). The predicted amino acid sequence disclosed herein for vo24\_1 was searched against the GenPept and GeneSeq  
15 amino acid sequence databases using the BLASTX search protocol. The predicted vo24\_1 protein demonstrated at least some similarity to sequences identified as W58774 (Human breast cancer gene CH1-9a11-2 protein fragment #1). Based upon sequence similarity, vo24\_1 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of vo24\_1 indicates that it may contain one or more of the following  
20 repetitive elements: Alu, Mer33.

#### Clone "vo25\_1"

          A polynucleotide of the present invention has been identified as clone "vo25\_1". vo25\_1 was isolated from a human adult pancreas cDNA library and was identified as  
25 encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo25\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vo25\_1 protein").

          The nucleotide sequence of vo25\_1 as presently determined is reported in SEQ ID NO:75, and includes a poly(A) tail. What applicants presently believe to be the proper  
30 reading frame and the predicted amino acid sequence of the vo25\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:76. Amino acids 11 to 23

of SEQ ID NO:76 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 24.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vo25\_1 should be approximately 1200 bp.

5       The nucleotide sequence disclosed herein for vo25\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vo25\_1 demonstrated at least some similarity with sequences identified as AI300566 (qn56a09.x1 NCI\_CGAP\_Kid5 Homo sapiens cDNA clone IMAGE 1902232 3' similar to WP C35D10.1 CE01190 ;, mRNA sequence), V34218  
10 (Human secreted protein gene 65 clone HSREG44), and Z55702 (H.sapiens CpG island DNA genomic MseI fragment, clone 58e10, forward read cpg58e10.ft1a). The predicted amino acid sequence disclosed herein for vo25\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vo25\_1 protein demonstrated at least some similarity to sequences identified as  
15 U21324 (similar to S. cerevisiae hypothetical protein YKL166 [Caenorhabditis elegans]) and W57893 (Protein of clone AT340\_1). Based upon sequence similarity, vo25\_1 proteins and each similar protein or peptide may share at least some activity. Motifs analysis detected an ATP/GTP-binding site motif A (P-loop) centered around residue 229 of SEQ ID NO:76. The TopPredII computer program predicts a potential transmembrane  
20 domain within the vo25\_1 protein sequence centered around amino acid 170 of SEQ ID NO:76.

#### Clone "vo26\_1"

A polynucleotide of the present invention has been identified as clone "vo26\_1".  
25 vo26\_1 was isolated from a human adult pancreas cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo26\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vo26\_1 protein").

The nucleotide sequence of vo26\_1 as presently determined is reported in SEQ ID  
30 NO:77, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vo26\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:78. Amino acids 13 to 25

of SEQ ID NO:78 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 26.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vo26\_1 should be approximately 2503 bp.

5        The nucleotide sequence disclosed herein for vo26\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vo26\_1 demonstrated at least some similarity with sequences identified as AC004707 (Homo sapiens chromosome 17, clone hRPC.117\_B\_12, complete sequence), AI160442 (qc08g02.x1 Soares\_fetal\_heart\_NbHH19W Homo sapiens cDNA  
10   clone IMAGE 1709042 3' similar to SW RM02\_YEAST P12687 MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L2 PRECURSOR; mRNA sequence), and T23473 (Human gene signature HUMGS05312). The predicted amino acid sequence disclosed herein for vo26\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vo26\_1 protein demonstrated at least  
15   some similarity to sequences identified as L37877 (ribosomal protein L27 [Filobasidiella neoformans]). Based upon sequence similarity, vo26\_1 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of vo26\_1 indicates that it may contain a Mir repeat.

20        Clone "vp23\_1"

A polynucleotide of the present invention has been identified as clone "vp23\_1". vp23\_1 was isolated from a human adult prostate cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vp23\_1 is a full-length clone, including the  
25   entire coding sequence of a secreted protein (also referred to herein as "vp23\_1 protein").

The nucleotide sequence of vp23\_1 as presently determined is reported in SEQ ID NO:79, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vp23\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:80. Amino acids 5 to 17  
30   of SEQ ID NO:80 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 18. Due to the hydrophobic nature of the predicted

leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vp23\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vp23\_1 should be approximately 1220 bp.

5        The nucleotide sequence disclosed herein for vp23\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vp23\_1 demonstrated at least some similarity with sequences identified as AL021578 (Human DNA sequence from clone 453C12 on chromosome 20q12-13.12 Contains SDC4 (syndecan 4 (amphiglycan, ryudocan)), predicts a gene like  
10       the mouse transcription factor RBP-L). Based upon sequence similarity, vp23\_1 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of vp23\_1 indicates that it may contain an Alu repetitive element.

Clone "vq7\_1"

15       A polynucleotide of the present invention has been identified as clone "vq7\_1". vq7\_1 was isolated from a human adult lung cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vq7\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vq7\_1 protein").

20       The nucleotide sequence of vq7\_1 as presently determined is reported in SEQ ID NO:81, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vq7\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:82. Amino acids 9 to 21 of SEQ ID NO:82 are a predicted leader/signal sequence, with the predicted mature amino  
25       acid sequence beginning at amino acid 22. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vq7\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vq7\_1 should be approximately 1326 bp.

30       The nucleotide sequence disclosed herein for vq7\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vq7\_1 demonstrated at least some similarity with sequences



identified as AA036918 (zk32e03.r1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 484540 5', mRNA sequence). The predicted amino acid sequence disclosed herein for vq7\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vq7\_1 protein demonstrated at least  
5 some similarity to sequences identified as AF142780 (butyrophilin-like protein [Mus musculus]). Butyrophilin is a glycoprotein of the immunoglobulin superfamily that is secreted in association with the milk-fat-globule membrane from mammary epithelial cells (Ogg *et al.*, 1996, *Mamm. Genome* 7 (12): 900-905, which is incorporated by reference herein). Based upon sequence similarity, vq7\_1 proteins and each similar protein or  
10 peptide may share at least some activity. The nucleotide sequence of vq7\_1 indicates that it may contain a repetitive element.

#### Clone "vq8\_1"

A polynucleotide of the present invention has been identified as clone "vq8\_1".  
15 vq8\_1 was isolated from a human adult lung cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vq8\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vq8\_1 protein").

The nucleotide sequence of vq8\_1 as presently determined is reported in SEQ ID  
20 NO:83, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vq8\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:84. Amino acids 10 to 22 of SEQ ID NO:84 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 23. Due to the hydrophobic nature of the predicted  
25 leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vq8\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vq8\_1 should be approximately 695 bp.

The nucleotide sequence disclosed herein for vq8\_1 was searched against the  
30 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vq8\_1 demonstrated at least some similarity with sequences identified as AA433968 (zw23f07.r1 Soares ovary tumor NbHOT Homo sapiens cDNA

clone 770149 5', mRNA sequence) and V69618 (Human secreted protein gene 8 clone HLHCM89). The predicted amino acid sequence disclosed herein for vq8\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vq8\_1 protein demonstrated at least some similarity to sequences identified as W83953 (Polypeptide encoded by gene 7 clone HJPDJ64). Based upon sequence similarity, vq8\_1 proteins and each similar protein or peptide may share at least some activity.

#### Clone "vq9\_1"

10 A polynucleotide of the present invention has been identified as clone "vq9\_1". vq9\_1 was isolated from a human adult lung cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vq9\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vq9\_1 protein").

15 The nucleotide sequence of vq9\_1 as presently determined is reported in SEQ ID NO:85, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vq9\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:86. Amino acids 5 to 17 of SEQ ID NO:86 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 18. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vq9\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vq9\_1 should be approximately 1218 bp.

25 The nucleotide sequence disclosed herein for vq9\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vq9\_1 demonstrated at least some similarity with sequences identified as AA769310 (nz39f03.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA clone IMAGE:1290173, mRNA sequence). The predicted amino acid sequence disclosed herein for vq9\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vq9\_1 protein demonstrated at least some similarity to sequences identified as U79260 (unknown [Homo sapiens]) and

W48351 (Human breast cancer related protein BCRB2). Based upon sequence similarity, vq9\_1 proteins and each similar protein or peptide may share at least some activity.

Clone "vq10\_1"

5           A polynucleotide of the present invention has been identified as clone "vq10\_1". vq10\_1 was isolated from a human adult lung cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vq10\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vq10\_1 protein").

10           The nucleotide sequence of vq10\_1 as presently determined is reported in SEQ ID NO:87, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vq10\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:88. Amino acids 6 to 18 of SEQ ID NO:88 are a predicted leader/signal sequence, with the predicted mature amino  
15           acid sequence beginning at amino acid 19. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vq10\_1 protein.

          Another potential reading frame, encoded by nucleotides 331 to 834 of SEQ ID NO:87, is reported as the amino acid sequence of SEQ ID NO:190. Amino acids 29 to 41  
20           of SEQ ID NO:190 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 42. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein of SEQ ID NO:190.

25           If one nucleotide was deleted from the group of nucleotides at positions 330 and 331 of SEQ ID NO:87, another potential reading frame would be created from what would then be nucleotides 18 to 836, with a predicted amino acid sequence reported as SEQ ID NO:191. Amino acids 6 to 18 of SEQ ID NO:191 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 19. Due to the  
30           hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein of SEQ ID NO:191.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vq10\_1 should be approximately 1516 bp.

The nucleotide sequence disclosed herein for vq10\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vq10\_1 demonstrated at least some similarity with sequences identified as AA359702 (EST68843 Fetal lung II Homo sapiens cDNA 5' end similar to similar to pulmonary surfactant protein B, mRNA sequence), I08571 (Sequence 14 from Patent WO 8706588), and Q79287 (Human pulmonary surfactant protein B (SPB)). The predicted amino acid sequence disclosed herein for vq10\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vq10\_1 protein demonstrated at least some similarity to sequences identified as J02761 (pulmonary surfactant-associated protein SP-B [Homo sapiens]) and P70664 (6kd pulmonary surfactant protein). Pulmonary surfactant associated proteins such as SP-B promote alveolar stability by lowering the surface tension at the air-liquid interface in the peripheral air spaces. Based upon sequence similarity, vq10\_1 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of vq10\_1 indicates that it may contain an Alu repetitive element.

#### Clone "vq13\_1"

A polynucleotide of the present invention has been identified as clone "vq13\_1". vq13\_1 was isolated from a human adult lung cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vq13\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vq13\_1 protein").

The nucleotide sequence of vq13\_1 as presently determined is reported in SEQ ID NO:89, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vq13\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:90. Amino acids 10 to 22 of SEQ ID NO:90 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 23. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vq13\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vq13\_1 should be approximately 2284 bp.

The nucleotide sequence disclosed herein for vq13\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vq13\_1 demonstrated at least some similarity with sequences identified as AA928678 (on48e07.s1 NCI\_CGAP\_Co8 Homo sapiens cDNA clone IMAGE 1559940 3', mRNA sequence), AB023187 (Homo sapiens mRNA for KIAA0970 protein, complete cds), and T19039 (Human gene signature HUMGS00046). Based upon sequence similarity, vq13\_1 proteins and each similar protein or peptide may share at least some activity.

#### Clone "vq16\_1"

A polynucleotide of the present invention has been identified as clone "vq16\_1". vq16\_1 was isolated from a human adult lung cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vq16\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vq16\_1 protein").

The nucleotide sequence of vq16\_1 as presently determined is reported in SEQ ID NO:91, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vq16\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:92. Amino acids 34 to 46 of SEQ ID NO:92 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 47. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the leader/signal sequence not be separated from the remainder of the vq16\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vq16\_1 should be approximately 1087 bp.

The nucleotide sequence disclosed herein for vq16\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vq16\_1 demonstrated at least some similarity with sequences identified as AA400700 (zu70g11.r1 Soares\_testis\_NHT Homo sapiens cDNA clone IMAGE:743396 5' similar to WP:R05D3.2 CE00281; mRNA sequence). The predicted

amino acid sequence disclosed herein for vq16\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vq16\_1 protein demonstrated at least some similarity to sequences identified as AF05611 (unknown [Fugu rubripes]). Based upon sequence similarity, vq16\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts three additional potential transmembrane domains within the vq16\_1 protein sequence, centered around amino acids 90, 134, and 174 of SEQ ID NO:92, respectively.

10        Clone "vq19\_1"

A polynucleotide of the present invention has been identified as clone "vq19\_1". vq19\_1 was isolated from a human adult lung cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vq19\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vq19\_1 protein").

The nucleotide sequence of vq19\_1 as presently determined is reported in SEQ ID NO:93, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vq19\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:94. Amino acids 11 to 23 of SEQ ID NO:94 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 24. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vq19\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vq19\_1 should be approximately 1833 bp.

The nucleotide sequence disclosed herein for vq19\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vq19\_1 demonstrated at least some similarity with sequences identified as AA577696 (nn22h03.s1 NCI\_CGAP\_Co12 Homo sapiens cDNA clone IMAGE:1084661 3' similar to contains Alu repetitive element; mRNA sequence. Based upon sequence similarity, vq19\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts an additional potential

transmembrane domains within the vq19\_1 protein sequence centered around amino acid 214 of SEQ ID NO:94. The nucleotide sequence of vq19\_1 indicates that it may contain an Alu repetitive element.

5           Clone "vq20\_1"

A polynucleotide of the present invention has been identified as clone "vq20\_1". vq20\_1 was isolated from a human adult lung cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vq20\_1 is a full-length clone, including the  
10   entire coding sequence of a secreted protein (also referred to herein as "vq20\_1 protein").

The nucleotide sequence of vq20\_1 as presently determined is reported in SEQ ID NO:95, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vq20\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:96. Amino acids 10 to 22  
15   of SEQ ID NO:96 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 23. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vq20\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone  
20   vq20\_1 should be approximately 1275 bp.

The nucleotide sequence disclosed herein for vq20\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vq20\_1 demonstrated at least some similarity with sequences identified as AA826249 (of11c04.s1 NCI\_CGAP\_Co12 Homo sapiens cDNA clone  
25   IMAGE 1420806 3' similar to TR Q13445 Q13445 PUTATIVE T1/ST2 RECEPTOR BINDING PROTEIN PRECURSOR; mRNA sequence), AI129838 (qc49h11.x1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone IMAGE:1712997 3' similar to TR:Q13445 Q13445 PUTATIVE T1/ST2 RECEPTOR BINDING PROTEIN PRECURSOR; mRNA sequence), U41805 (Mus musculus putative T1/ST2 receptor  
30   binding protein precursor mRNA, partial cds), and V17729 (Human T1 receptor-like ligand II cDNA). The predicted amino acid sequence disclosed herein for vq20\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the

BLASTX search protocol. The predicted vq20\_1 protein demonstrated at least some similarity to sequences identified as U41804 (putative T1/ST2 receptor binding protein precursor [Homo sapiens]) and W48335 (Human T1 receptor-like ligand II). T1/ST2 is a receptor-like molecule homologous to the type I interleukin-1 receptor (Gayle *et al.*,  
5 1996, *J. Biol. Chem.* **271** (10): 5784-5789, which is incorporated by reference herein). Based upon sequence similarity, vq20\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts an additional potential transmembrane domain within the vq20\_1 protein sequence centered around amino acid 208 of SEQ ID NO:96.

10

#### Clone "vq21\_1"

A polynucleotide of the present invention has been identified as clone "vq21\_1". vq21\_1 was isolated from a human adult lung cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the  
15 amino acid sequence of the encoded protein. vq21\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vq21\_1 protein").

The nucleotide sequence of vq21\_1 as presently determined is reported in SEQ ID NO:97, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vq21\_1 protein corresponding  
20 to the foregoing nucleotide sequence is reported in SEQ ID NO:98. Amino acids 16 to 28 of SEQ ID NO:98 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 29. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vq21\_1 protein.

25 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vq21\_1 should be approximately 1230 bp.

The nucleotide sequence disclosed herein for vq21\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vq21\_1 demonstrated at least some similarity with sequences  
30 identified as AA149768 (zo01g05.s1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE 566456 3' similar to contains Alu repetitive element; mRNA sequence), AC005282 (Homo sapiens clone DJ0826E18, WORKING DRAFT SEQUENCE, 4



unordered pieces), T25413 (Human gene signature HUMGS07579). The predicted amino acid sequence disclosed herein for vq21\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vq21\_1 protein demonstrated at least some similarity to sequences identified as U67577 (cell  
5 division protein FtsJ [Methanococcus jannaschii]). Based upon sequence similarity, vq21\_1 proteins and each similar protein or peptide may share at least some activity.

#### Clone "vr2\_1"

A polynucleotide of the present invention has been identified as clone "vr2\_1".  
10 vr2\_1 was isolated from a human adult lung cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vr2\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vr2\_1 protein").

The nucleotide sequence of vr2\_1 as presently determined is reported in SEQ ID  
15 NO:99. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vr2\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:100.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone  
vr2\_1 should be approximately 1382 bp.

20 The nucleotide sequence disclosed herein for vr2\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No significant similarities were identified in the databases. The TopPredII computer program predicts a potential transmembrane domain within the vr2\_1 protein sequence centered around amino acid 85 of SEQ ID NO:100. The nucleotide  
25 sequence of vr2\_1 indicates that it may contain one or more of the following repetitive elements: Alu, MER2, MER4B.

#### Clone "vc69\_1"

A polynucleotide of the present invention has been identified as clone "vc69\_1".  
30 vc69\_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the

amino acid sequence of the encoded protein. vc69\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vc69\_1 protein").

The nucleotide sequence of vc69\_1 as presently determined is reported in SEQ ID NO:101, and includes a poly(A) tail. What applicants presently believe to be the proper  
5 reading frame and the predicted amino acid sequence of the vc69\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:102. Amino acids 7 to 19 of SEQ ID NO:102 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 20. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the  
10 predicted leader/signal sequence not be separated from the remainder of the vc69\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vc69\_1 should be approximately 1600 bp.

The nucleotide sequence disclosed herein for vc69\_1 was searched against the  
15 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vc69\_1 demonstrated at least some similarity with sequences identified as AB023138 (Homo sapiens mRNA for KIAA0921 protein, partial cds), and AI421941 (tf45c01.x1 NCI\_CGAP\_Brn23 Homo sapiens cDNA clone IMAGE 2099136 3' similar to TR Q63376 Q63376 NEUREXIN II-BETA-A PRECURSOR; mRNA  
20 sequence). The predicted amino acid sequence disclosed herein for vc69\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vc69\_1 protein demonstrated at least some similarity to sequences identified as AB02313 (KIAA0921 protein [Homo sapiens]), and various isoforms of *Rattus norvegicus* neurexin II protein. Based upon sequence similarity,  
25 vc69\_1 proteins and each similar protein or peptide may share at least some activity.

#### Clone "vc71\_1"

A polynucleotide of the present invention has been identified as clone "vc71\_1". vc71\_1 was isolated from a human fetal brain cDNA library and was identified as  
30 encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vc71\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vc71\_1 protein").

The nucleotide sequence of vc71\_1 as presently determined is reported in SEQ ID NO:103, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vc71\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:104. Amino acids 2 to 14 of SEQ ID NO:104 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 15. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vc71\_1 protein.

10 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vc71\_1 should be approximately 760 bp.

The nucleotide sequence disclosed herein for vc71\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vc71\_1 demonstrated at least some similarity with sequences identified as AI393859 (tg65f04.x1 Soares\_NhHMPu\_S1 Homo sapiens cDNA clone IMAGE 2113663 3', mRNA sequence) and AL050018 (Homo sapiens mRNA; cDNA DKFZp564B116 (from clone DKFZp564B116)). Based upon sequence similarity, vc71\_1 proteins and each similar protein or peptide may share at least some activity.

20 Clone "vo27\_1"

A polynucleotide of the present invention has been identified as clone "vo27\_1". vo27\_1 was isolated from a human adult pancreas cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo27\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vo27\_1 protein").

The nucleotide sequence of vo27\_1 as presently determined is reported in SEQ ID NO:105, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vo27\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:106. Amino acids 13 to 25 of SEQ ID NO:106 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 26. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the

predicted leader/signal sequence not be separated from the remainder of the vo27\_1 protein.

Another potential reading frame, encoded by nucleotides 1665 to 1844 of SEQ ID NO:105, is reported as the amino acid sequence of SEQ ID NO:192. Amino acids 4 to 16 of SEQ ID NO:192 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 17; amino acids 28 to 40 of SEQ ID NO:192 are also a possible leader/signal sequence, with the predicted mature amino acid sequence beginning in that case at amino acid 41. Due to the hydrophobic nature of these predicted leader/signal sequences, each is likely to act as a transmembrane domain should it not be separated from the remainder of the protein of SEQ ID NO:192.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vo27\_1 should be approximately 2433 bp.

The nucleotide sequence disclosed herein for vo27\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vo27\_1 demonstrated at least some similarity with sequences identified as AC007621 (Homo sapiens clone RPCI11-757G14, WORKING DRAFT SEQUENCE, 142 unordered pieces), AI207832 (ao89g11.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE 1953092 3' similar to contains Alu repetitive element; mRNA sequence), and X80059 (Human PRO361 nucleotide sequence). Based upon sequence similarity, vo27\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the vo27\_1 protein sequence centered around amino acid 400 of SEQ ID NO:106. The nucleotide sequence of vo27\_1 indicates that it may contain an Alu repetitive element.

#### Clone "vo31\_1"

A polynucleotide of the present invention has been identified as clone "vo31\_1". vo31\_1 was isolated from a human adult pancreas cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo31\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vo31\_1 protein").

The nucleotide sequence of vo31\_1 as presently determined is reported in SEQ ID NO:107, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vo31\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:108. Amino acids 7 to 19 of SEQ ID NO:108 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 20. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vo31\_1 protein.

10 Another potential reading frame, encoded by nucleotides 1937 to 3007 of SEQ ID NO:107, is reported as the amino acid sequence of SEQ ID NO:193.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vo31\_1 should be approximately 3222 bp.

The nucleotide sequence disclosed herein for vo31\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vo31\_1 demonstrated at least some similarity with sequences identified as AF022147 (*Rattus norvegicus* uterus-ovary specific putative transmembrane protein (uo) mRNA, complete cds), AI417638 (tg80e01.x1 Soares\_NhHMPu\_S1 *Homo sapiens* cDNA clone IMAGE 2115096 3' similar to TR O35360 O35360 UTERUS-OVARY SPECIFIC PUTATIVE TRANSMEMBRANE PROTEIN; mRNA sequence), and X52248 (Protein PRO257 cDNA clone DNA35841-1173). The predicted amino acid sequence disclosed herein for vo31\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vo31\_1 protein demonstrated at least some similarity to sequences identified as AF02214 (uterus-ovary specific putative transmembrane protein [*Rattus norvegicus*]) and Y13377 (Amino acid sequence of protein PRO257). Based upon sequence similarity, vo31\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the protein sequence of SEQ ID NO:193, centered around amino acid 328 of SEQ ID NO:193.

25 Hidden markov model analysis indicates the presence of Zona-pellucida-like domains at amino acids 26-115 and 146-273 of SEQ ID NO:193. The nucleotide sequence of vo31\_1 indicates that it may contain a Mer5a repetitive element.

30

Clone "vo32\_1"

A polynucleotide of the present invention has been identified as clone "vo32\_1". vo32\_1 was isolated from a human adult pancreas cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo32\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vo32\_1 protein").

The nucleotide sequence of vo32\_1 as presently determined is reported in SEQ ID NO:109, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vo32\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:110. Amino acids 4 to 16 of SEQ ID NO:110 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 17. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vo32\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vo32\_1 should be approximately 1868 bp.

The nucleotide sequence disclosed herein for vo32\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vo32\_1 demonstrated at least some similarity with sequences identified as AF028740 (Mus musculus olfactomedin mRNA, complete cds), AJ078144 (oz30b06.x1 Soares\_total\_fetus\_Nb2HF8\_9w Homo sapiens cDNA clone IMAGE 1676819 3' similar to TR Q99784 Q99784 NEURONAL OLFACTOMEDIN-RELATED ER LOCALIZED PROTEIN; mRNA sequence), AI869993 (wl63e09.x1 NCI\_CGAP Brn25 Homo sapiens cDNA clone IMAGE:2429608 3' similar to SW:NOMR\_HUMAN Q99784 NEURONAL OLFACTOMEDIN-RELATED ER LOCALIZED PROTEIN; mRNA sequence), and V34217 (Human secreted protein gene 64 clone HSLDJ95). The predicted amino acid sequence disclosed herein for vo32\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vo32\_1 protein demonstrated at least some similarity to sequences identified as U03416 (neuronal olfactomedin-related ER localized protein [Rattus norvegicus]) and W75120 (Human secreted protein encoded by gene 64 clone HSLDJ95). Based upon

sequence similarity, vo32\_1 proteins and each similar protein or peptide may share at least some activity.

Clone "vo33\_1"

5 A polynucleotide of the present invention has been identified as clone "vo33\_1". vo33\_1 was isolated from a human adult pancreas cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo33\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vo33\_1 protein").

10 The nucleotide sequence of vo33\_1 as presently determined is reported in SEQ ID NO:111, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vo33\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:112. Amino acids 5 to 17 of SEQ ID NO:112 are a predicted leader/signal sequence, with the predicted mature  
15 amino acid sequence beginning at amino acid 18. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vo33\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone  
20 vo33\_1 should be approximately 2879 bp.

The nucleotide sequence disclosed herein for vo33\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vo33\_1 demonstrated at least some similarity with sequences identified as AI225613 (uj13e01.y1 Sugano mouse kidney mkia Mus musculus cDNA  
25 clone IMAGE:1907928 5' similar to TR:Q14624 Q14624 INTER-ALPHA-TRYPSIN INHIBITOR FAMILY HEAVY CHAIN-RELATED PROTEIN; mRNA sequence) and X80054 (Human PRO354 nucleotide sequence). The predicted amino acid sequence disclosed herein for vo33\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vo33\_1 protein  
30 demonstrated at least some similarity to sequences identified as D38535 (PK-120 precursor [Homo sapiens]), Y11545 (inter-alpha-inhibitor heavy-chain H2 [Sus scrofa]), and the H2 proteins of several species, including *Homo sapiens*. Based upon sequence similarity,

vo33\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the vo33\_1 protein sequence centered around amino acid 386 of SEQ ID NO:112. The nucleotide sequence of vo33\_1 indicates that it may contain an Alu repetitive element.

5

Clone "vq23\_1"

A polynucleotide of the present invention has been identified as clone "vq23\_1". vq23\_1 was isolated from a human adult lung cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vq23\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vq23\_1 protein").

The nucleotide sequence of vq23\_1 as presently determined is reported in SEQ ID NO:113, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vq23\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:114. Amino acids 18 to 30 of SEQ ID NO:114 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 31. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vq23\_1 protein.

Another potential reading frame, encoded by nucleotides 1012 to 1518 of SEQ ID NO:113, is reported as the amino acid sequence of SEQ ID NO:194. Amino acids 83 to 94 of SEQ ID NO:194 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 95. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of protein of SEQ ID NO:194.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vq23\_1 should be approximately 1793 bp.

The nucleotide sequence disclosed herein for vq23\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vq23\_1 demonstrated at least some similarity with sequences



identified as AA625521 (af72f02.r1 Soares\_NhHMPu\_S1 Homo sapiens cDNA clone IMAGE 1047579 5', mRNA sequence) and AC002364 (Homo sapiens Xp22 Cosmids U15E4, U115H5, U132E12, U115B9 (Lawrence Livermore human cosmid library) complete sequence). Based upon sequence similarity, vq23\_1 proteins and each similar  
5 protein or peptide may share at least some activity. The nucleotide sequence of vq23\_1 indicates that it may contain an Alu repetitive element.

#### Clone "vq24\_1"

A polynucleotide of the present invention has been identified as clone "vq24\_1".  
10 vq24\_1 was isolated from a human adult lung cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vq24\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vq24\_1 protein").

The nucleotide sequence of vq24\_1 as presently determined is reported in SEQ ID  
15 NO:115, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vq24\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:116. Amino acids 5 to 17 of SEQ ID NO:116 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 18. Due to the hydrophobic nature of the  
20 predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vq24\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vq24\_1 should be approximately 2168 bp.

25 The nucleotide sequence disclosed herein for vq24\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vq24\_1 demonstrated at least some similarity with sequences identified as N29315 (yx43d06.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:264491 5' similar to SP:SW:FCG1\_HUMAN P12315 HIGH AFFINITY  
30 IMMUNOGLOBULIN GAMMA FC RECEPTOR I 'B FORM' PRECURSOR; mRNA sequence). The predicted amino acid sequence disclosed herein for vq24\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX

search protocol. The predicted vq24\_1 protein demonstrated at least some similarity to sequences identified as AF14317 (high affinity immunoglobulin gamma Fc receptor I [Mus musculus]) and R12428 (Hybrid Fc(gamma)RII/I receptor). Based upon sequence similarity, vq24\_1 proteins and each similar protein or peptide may share at least some activity. Hidden markov model analysis detects immunoglobulin superfamily signatures in the vq24\_1 protein sequence from amino acid 92 to amino acid 145, and from amino acid 185 to amino acid 242, of SEQ ID NO:116. The nucleotide sequence of vq24\_1 indicates that it may contain one or more of the following repetitive elements: Mer, MLT1a.

10

#### Clone "vq26\_1"

A polynucleotide of the present invention has been identified as clone "vq26\_1". vq26\_1 was isolated from a human adult lung cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vq26\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vq26\_1 protein").

The nucleotide sequence of vq26\_1 as presently determined is reported in SEQ ID NO:117, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vq26\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:118. Amino acids 9 to 21 of SEQ ID NO:118 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 22. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vq26\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vq26\_1 should be approximately 1419 bp.

The nucleotide sequence disclosed herein for vq26\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vq26\_1 demonstrated at least some similarity with sequences identified as AA191552 (zp82g04.s1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE 626742 3', mRNA sequence) and AA573741 (nk07a05.s1 NCI\_CGAP\_Co2

Homo sapiens cDNA clone IMAGE:1012784 3', mRNA sequence). Based upon sequence similarity, vq26\_1 proteins and each similar protein or peptide may share at least some activity.

5        Deposit of Clones

Clones vc62\_1, vp10\_1, vp11\_1, vp13\_1, vp16\_1, vp21\_1, vp22\_1, vq2\_1, vq3\_1, vq5\_1, vq6\_1, and vr1\_1 were deposited on February 17, 1999 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession  
10        number ATCC 207114, from which each clone comprising a particular polynucleotide is obtainable.

Clone vc63\_1 was deposited on February 17, 1999 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and was given the accession  
15        ATCC 207115, from which the vc63\_1 clone comprising a particular polynucleotide is obtainable.

Clones vb25\_1, vb27\_1, vb28\_1, vb29\_1, vb30\_1, vc67\_1, vf4\_1, vg3\_1, vo2\_1, vo3\_1, vo5\_1, vo6\_1, and vo9\_1 were deposited on July 15, 1999 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia  
20        20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number PTA-362, from which each clone comprising a particular polynucleotide is obtainable.

Clones vol1\_1, vol2\_1, vol3\_1, vol4\_1, vol5\_1, vol6\_1, vol8\_1, vol9\_1, vol10\_1, vol11\_1, vol12\_1, vol13\_1, vol14\_1, vol15\_1, vol16\_1, vol18\_1, vol19\_1, vol20\_1, vol21\_1, vol22\_1, vol23\_1, vol24\_1, vol25\_1, and vol26\_1 were deposited on July 15, 1999 with the  
25        ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number PTA-366, from which each clone comprising a particular polynucleotide is obtainable.

Clones vp23\_1, vq7\_1, vq8\_1, vq9\_1, vq10\_1, vq13\_1, vq16\_1, vq19\_1, vq20\_1, vq21\_1, and vr2\_1 were deposited on July 15, 1999 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.)  
30

as an original deposit under the Budapest Treaty and were given the accession number PTA-368, from which each clone comprising a particular polynucleotide is obtainable.

Clones vc69\_1, vc71\_1, vo27\_1, vo31\_1, vo32\_1, vo33\_1, vq23\_1, vq24\_1, and vq26\_1 were deposited on December 21, 1999 with the ATCC (American Type Culture  
5 Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number PTA-1075, from which each clone comprising a particular polynucleotide is obtainable.

All restrictions on the availability to the public of the deposited material will be irrevocably removed upon the granting of the patent, except for the requirements specified  
10 in 37 C.F.R. § 1.808(b), and the term of the deposit will comply with 37 C.F.R. § 1.806.

Each clone has been transfected into separate bacterial cells (*E. coli*) in these composite deposits. Each clone can be removed from the vector in which it was deposited by performing an EcoRI/NotI digestion (5' site, EcoRI; 3' site, NotI) to produce the appropriate fragment for such clone. Each clone was deposited in either the pED6 or  
15 pNOTs vector depicted in Figures 1A and 1B, respectively. The pED6dpc2 vector ("pED6") was derived from pED6dpc1 by insertion of a new polylinker to facilitate cDNA cloning (Kaufman *et al.*, 1991, *Nucleic Acids Res.* 19: 4485-4490); the pNOTs vector was derived from pMT2 (Kaufman *et al.*, 1989, *Mol. Cell. Biol.* 9: 946-958) by deletion of the DHFR sequences, insertion of a new polylinker, and insertion of the M13  
20 origin of replication in the ClaI site. In some instances, the deposited clone can become "flipped" (i.e., in the reverse orientation) in the deposited isolate. In such instances, the cDNA insert can still be isolated by digestion with EcoRI and NotI. However, NotI will then produce the 5' site and EcoRI will produce the 3' site for placement of the cDNA in proper orientation for expression in a suitable vector. The cDNA may also be expressed  
25 from the vectors in which they were deposited.

Bacterial cells containing a particular clone can be obtained from the composite deposit as follows:

An oligonucleotide probe or probes should be designed to the sequence that is known for that particular clone. This sequence can be derived from the sequences  
30 provided herein, or from a combination of those sequences. The sequence of an oligonucleotide probe that was used to isolate or to sequence each full-length clone is identified below, and should be most reliable in isolating the clone of interest.

	<u>Clone</u>	<u>Probe Sequence</u>
	vc62_1	SEQ ID NO:119
	vp10_1	SEQ ID NO:120
	vp11_1	SEQ ID NO:121
5	vp13_1	SEQ ID NO:122
	vp16_1	SEQ ID NO:123
	vp21_1	SEQ ID NO:124
	vp22_1	SEQ ID NO:125
	vq2_1	SEQ ID NO:126
10	vq3_1	SEQ ID NO:127
	vq5_1	SEQ ID NO:128
	vq6_1	SEQ ID NO:129
	vr1_1	SEQ ID NO:130
	vc63_1	SEQ ID NO:131
15	vb25_1	SEQ ID NO:132
	vb27_1	SEQ ID NO:133
	vb28_1	SEQ ID NO:134
	vb29_1	SEQ ID NO:135
	vb30_1	SEQ ID NO:136
20	vc67_1	SEQ ID NO:137
	vf4_1	SEQ ID NO:138
	vg3_1	SEQ ID NO:139
	vo2_1	SEQ ID NO:140
	vo3_1	SEQ ID NO:141
25	vo5_1	SEQ ID NO:142
	vo6_1	SEQ ID NO:143
	vo9_1	SEQ ID NO:144
	vol1_1	SEQ ID NO:145
	vol2_1	SEQ ID NO:146
30	vol3_1	SEQ ID NO:147
	vol4_1	SEQ ID NO:148
	vol5_1	SEQ ID NO:149

	vol6_1	SEQ ID NO:150
	vol8_1	SEQ ID NO:151
	vol9_1	SEQ ID NO:152
	vo22_1	SEQ ID NO:153
5	vo23_1	SEQ ID NO:154
	vo24_1	SEQ ID NO:155
	vo25_1	SEQ ID NO:156
	vo26_1	SEQ ID NO:157
	vp23_1	SEQ ID NO:158
10	vq7_1	SEQ ID NO:159
	vq8_1	SEQ ID NO:160
	vq9_1	SEQ ID NO:161
	vq10_1	SEQ ID NO:162
	vq13_1	SEQ ID NO:163
15	vq16_1	SEQ ID NO:164
	vq19_1	SEQ ID NO:165
	vq20_1	SEQ ID NO:166
	vq21_1	SEQ ID NO:167
	vr2_1	SEQ ID NO:168

20

In the sequences listed above which include an N at position 2, that position is occupied in preferred probes/primers by a biotinylated phosphoramidite residue rather than a nucleotide (such as, for example, that produced by use of biotin phosphoramidite (1-dimethoxytrityloxy-2-(N-biotinyl-4-aminobutyl)-propyl-3-O-(2-cyanoethyl)-(N,N-diisopropyl)-phosphoramidite) (Glen Research, cat. no. 10-1953)).

25

The design of the oligonucleotide probe should preferably follow these parameters:

- (a) It should be designed to an area of the sequence which has the fewest ambiguous bases ("N's"), if any;
- (b) It should be designed to have a  $T_m$  of approx. 80 ° C (assuming 2° for each A or T and 4 degrees for each G or C).

30

The oligonucleotide should preferably be labeled with  $\gamma$ - $^{32}\text{P}$  ATP (specific activity 6000 Ci/mmol) and T4 polynucleotide kinase using commonly employed techniques for

labeling oligonucleotides. Other labeling techniques can also be used. Unincorporated label should preferably be removed by gel filtration chromatography or other established methods. The amount of radioactivity incorporated into the probe should be quantitated by measurement in a scintillation counter. Preferably, specific activity of the resulting  
5 probe should be approximately  $4 \times 10^6$  dpm/pmole.

The bacterial culture containing the pool of full-length clones should preferably be thawed and 100  $\mu$ l of the stock used to inoculate a sterile culture flask containing 25 ml of sterile L-broth containing ampicillin at 100  $\mu$ g/ml. The culture should preferably be grown to saturation at 37°C, and the saturated culture should preferably be diluted in fresh  
10 L-broth. Aliquots of these dilutions should preferably be plated to determine the dilution and volume which will yield approximately 5000 distinct and well-separated colonies on solid bacteriological media containing L-broth containing ampicillin at 100  $\mu$ g/ml and agar at 1.5% in a 150 mm petri dish when grown overnight at 37°C. Other known methods of obtaining distinct, well-separated colonies can also be employed.

15 Standard colony hybridization procedures should then be used to transfer the colonies to nitrocellulose filters and lyse, denature and bake them.

The filter is then preferably incubated at 65°C for 1 hour with gentle agitation in 6X SSC (20X stock is 175.3 g NaCl/liter, 88.2 g Na citrate/liter, adjusted to pH 7.0 with NaOH) containing 0.5% SDS, 100  $\mu$ g/ml of yeast RNA, and 10 mM EDTA  
20 (approximately 10 mL per 150 mm filter). Preferably, the probe is then added to the hybridization mix at a concentration greater than or equal to  $1 \times 10^6$  dpm/mL. The filter is then preferably incubated at 65°C with gentle agitation overnight. The filter is then preferably washed in 500 mL of 2X SSC/0.5% SDS at room temperature without agitation, preferably followed by 500 mL of 2X SSC/0.1% SDS at room temperature with gentle  
25 shaking for 15 minutes. A third wash with 0.1X SSC/0.5% SDS at 65°C for 30 minutes to 1 hour is optional. The filter is then preferably dried and subjected to autoradiography for sufficient time to visualize the positives on the X-ray film. Other known hybridization methods can also be employed.

The positive colonies are picked, grown in culture, and plasmid DNA isolated  
30 using standard procedures. The clones can then be verified by restriction analysis, hybridization analysis, or DNA sequencing.

Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, as described in H.U. Saragovi, *et al.*, *Bio/Technology* 10, 773-778 (1992) and in R.S. McDowell, *et al.*, *J. Amer. Chem. Soc.* 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites. For example, fragments of the protein may be fused through "linker" sequences to the Fc portion of an immunoglobulin. For a bivalent form of the protein, such a fusion could be to the Fc portion of an IgG molecule. Other immunoglobulin isotypes may also be used to generate such fusions. For example, a protein - IgM fusion would generate a decavalent form of the protein of the invention.

The present invention also provides both full-length and mature forms of the disclosed proteins. The full-length form of the such proteins is identified in the sequence listing by translation of the nucleotide sequence of each disclosed clone. The mature form(s) of such protein may be obtained by expression of the disclosed full-length polynucleotide (preferably those deposited with the ATCC) in a suitable mammalian cell or other host cell. The sequence(s) of the mature form(s) of the protein may also be determinable from the amino acid sequence of the full-length form.

The present invention also provides genes corresponding to the polynucleotide sequences disclosed herein. "Corresponding genes" are the regions of the genome that are transcribed to produce the mRNAs from which cDNA polynucleotide sequences are derived and may include contiguous regions of the genome necessary for the regulated expression of such genes. Corresponding genes may therefore include but are not limited to coding sequences, 5' and 3' untranslated regions, alternatively spliced exons, introns, promoters, enhancers, and silencer or suppressor elements. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. An "isolated gene" is a gene that has been separated from the adjacent coding sequences, if any, present in the genome of the organism from which the gene was isolated.



The chromosomal location corresponding to the polynucleotide sequences disclosed herein may also be determined, for example by hybridizing appropriately labeled polynucleotides of the present invention to chromosomes *in situ*. It may also be possible to determine the corresponding chromosomal location for a disclosed polynucleotide by identifying significantly similar nucleotide sequences in public databases, such as expressed sequence tags (ESTs), that have already been mapped to particular chromosomal locations. For at least some of the polynucleotide sequences disclosed herein, public database sequences having at least some similarity to the polynucleotide of the present invention have been listed by database accession number. Searches using the GenBank accession numbers of these public database sequences can then be performed at an Internet site provided by the National Center for Biotechnology Information having the address <http://www.ncbi.nlm.nih.gov/UniGene/>, in order to identify "UniGene clusters" of overlapping sequences. Many of the "UniGene clusters" so identified will already have been mapped to particular chromosomal sites.

Organisms that have enhanced, reduced, or modified expression of the gene(s) corresponding to the polynucleotide sequences disclosed herein are provided. The desired change in gene expression can be achieved through the use of antisense polynucleotides or ribozymes that bind and/or cleave the mRNA transcribed from the gene (Albert and Morris, 1994, *Trends Pharmacol. Sci.* **15**(7): 250-254; Lavarosky *et al.*, 1997, *Biochem. Mol. Med.* **62**(1): 11-22; and Hampel, 1998, *Prog. Nucleic Acid Res. Mol. Biol.* **58**: 1-39; all of which are incorporated by reference herein). The desired change in gene expression can also be achieved through the use of double-stranded ribonucleotide molecules having some complementarity to the mRNA transcribed from the gene, and which interfere with the transcription, stability, or expression of the mRNA ("RNA interference" or "RNAi"; Fire *et al.*, 1998, *Nature* **391** (6669): 806-811; Montgomery *et al.*, 1998, *Proc. Natl. Acad. Sci. USA* **95** (26): 15502-15507; and Sharp, 1999, *Genes Dev.* **13** (2): 139-141; all of which are incorporated by reference herein). Transgenic animals that have multiple copies of the gene(s) corresponding to the polynucleotide sequences disclosed herein, preferably produced by transformation of cells with genetic constructs that are stably maintained within the transformed cells and their progeny, are provided. Transgenic animals that have modified genetic control regions that increase or reduce gene expression levels, or that change temporal or spatial patterns of gene expression, are also provided (see European

Patent No. 0 649 464 B1, incorporated by reference herein). In addition, organisms are provided in which the gene(s) corresponding to the polynucleotide sequences disclosed herein have been partially or completely inactivated, through insertion of extraneous sequences into the corresponding gene(s) or through deletion of all or part of the corresponding gene(s). Partial or complete gene inactivation can be accomplished through insertion, preferably followed by imprecise excision, of transposable elements (Plasterk, 1992, *Bioessays* **14**(9): 629-633; Zwaal *et al.*, 1993, *Proc. Natl. Acad. Sci. USA* **90**(16): 7431-7435; Clark *et al.*, 1994, *Proc. Natl. Acad. Sci. USA* **91**(2): 719-722; all of which are incorporated by reference herein), or through homologous recombination, preferably detected by positive/negative genetic selection strategies (Mansour *et al.*, 1988, *Nature* **336**: 348-352; U.S. Patent Nos. 5,464,764; 5,487,992; 5,627,059; 5,631,153; 5,614,396; 5,616,491; and 5,679,523; all of which are incorporated by reference herein). These organisms with altered gene expression are preferably eukaryotes and more preferably are mammals. Such organisms are useful for the development of non-human models for the study of disorders involving the corresponding gene(s), and for the development of assay systems for the identification of molecules that interact with the protein product(s) of the corresponding gene(s).

Where the protein of the present invention is membrane-bound (e.g., is a receptor), the present invention also provides for soluble forms of such protein. In such forms, part or all of the intracellular and transmembrane domains of the protein are deleted such that the protein is fully secreted from the cell in which it is expressed. The intracellular and transmembrane domains of proteins of the invention can be identified in accordance with known techniques for determination of such domains from sequence information. For example, the TopPredII computer program can be used to predict the location of transmembrane domains in an amino acid sequence, domains which are described by the location of the center of the transmembrane domain, with at least ten transmembrane amino acids on each side of the reported central residue(s).

Proteins and protein fragments of the present invention include proteins with amino acid sequence lengths that are at least 25% (more preferably at least 50%, and most preferably at least 75%) of the length of a disclosed protein and have at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% or 95% identity) with that disclosed protein, where sequence identity is determined by comparing the amino acid

sequences of the proteins when aligned so as to maximize overlap and identity while minimizing sequence gaps. Also included in the present invention are proteins and protein fragments that contain a segment preferably comprising 8 or more (more preferably 20 or more, most preferably 30 or more) contiguous amino acids that shares at least 75% sequence identity (more preferably, at least 85% identity; most preferably at least 95% identity) with any such segment of any of the disclosed proteins.

In particular, sequence identity may be determined using WU-BLAST (Washington University BLAST) version 2.0 software, which builds upon WU-BLAST version 1.4, which in turn is based on the public domain NCBI-BLAST version 1.4 (Altschul and Gish, 1996, Local alignment statistics, Doolittle *ed.*, *Methods in Enzymology* **266**: 460-480; Altschul *et al.*, 1990, Basic local alignment search tool, *Journal of Molecular Biology* **215**: 403-410; Gish and States, 1993, Identification of protein coding regions by database similarity search, *Nature Genetics* **3**: 266-272; Karlin and Altschul, 1993, Applications and statistics for multiple high-scoring segments in molecular sequences, *Proc. Natl. Acad. Sci. USA* **90**: 5873-5877; all of which are incorporated by reference herein). WU-BLAST version 2.0 executable programs for several UNIX platforms can be downloaded from <ftp://blast.wustl.edu/blast/executables>. The complete suite of search programs (BLASTP, BLASTN, BLASTX, TBLASTN, and TBLASTX) is provided at that site, in addition to several support programs. WU-BLAST 2.0 is copyrighted and may not be sold or redistributed in any form or manner without the express written consent of the author; but the posted executables may otherwise be freely used for commercial, nonprofit, or academic purposes. In all search programs in the suite -- BLASTP, BLASTN, BLASTX, TBLASTN and TBLASTX -- the gapped alignment routines are integral to the database search itself, and thus yield much better sensitivity and selectivity while producing the more easily interpreted output. Gapping can optionally be turned off in all of these programs, if desired. The default penalty (Q) for a gap of length one is Q=9 for proteins and BLASTP, and Q=10 for BLASTN, but may be changed to any integer value including zero, one through eight, nine, ten, eleven, twelve through twenty, twenty-one through fifty, fifty-one through one hundred, etc. The default per-residue penalty for extending a gap (R) is R=2 for proteins and BLASTP, and R=10 for BLASTN, but may be changed to any integer value including zero, one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve through twenty, twenty-one through fifty, fifty-one through one hundred, etc. Any

combination of values for Q and R can be used in order to align sequences so as to maximize overlap and identity while minimizing sequence gaps. The default amino acid comparison matrix is BLOSUM62, but other amino acid comparison matrices such as PAM can be utilized.

5 Species homologues of the disclosed polynucleotides and proteins are also provided by the present invention. As used herein, a "species homologue" is a protein or polynucleotide with a different species of origin from that of a given protein or polynucleotide, but with significant sequence similarity to the given protein or polynucleotide. Preferably, polynucleotide species homologues have at least 60% sequence  
10 identity (more preferably, at least 75% identity; most preferably at least 90% identity) with the given polynucleotide, and protein species homologues have at least 30% sequence identity (more preferably, at least 45% identity; most preferably at least 60% identity) with the given protein, where sequence identity is determined by comparing the nucleotide sequences of the polynucleotides or the amino acid sequences of the proteins when aligned so as to maximize  
15 overlap and identity while minimizing sequence gaps. Species homologues may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species. Preferably, species homologues are those isolated from mammalian species. Most preferably, species homologues are those isolated from certain mammalian species such as, for example, *Pan troglodytes*, *Gorilla*  
20 *gorilla*, *Pongo pygmaeus*, *Hylobates concolor*, *Macaca mulatta*, *Papio papio*, *Papio hamadryas*, *Cercopithecus aethiops*, *Cebus capucinus*, *Aotus trivirgatus*, *Sanguinus oedipus*, *Microcebus murinus*, *Mus musculus*, *Rattus norvegicus*, *Cricetulus griseus*, *Felis catus*, *Mustela vison*, *Canis familiaris*, *Oryctolagus cuniculus*, *Bos taurus*, *Ovis aries*, *Sus scrofa*, and *Equus caballus*, for which genetic maps have been created allowing the  
25 identification of syntenic relationships between the genomic organization of genes in one species and the genomic organization of the related genes in another species (O'Brien and Seuáñez, 1988, *Ann. Rev. Genet.* 22: 323-351; O'Brien *et al.*, 1993, *Nature Genetics* 3:103-112; Johansson *et al.*, 1995, *Genomics* 25: 682-690; Lyons *et al.*, 1997, *Nature Genetics* 15: 47-56; O'Brien *et al.*, 1997, *Trends in Genetics* 13(10): 393-399; Carver and  
30 Stubbs, 1997, *Genome Research* 7:1123-1137; all of which are incorporated by reference herein).

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotides which also encode proteins which are identical or have significantly similar sequences to those encoded by the disclosed polynucleotides. Preferably, allelic variants have at least  
5 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% identity) with the given polynucleotide, where sequence identity is determined by comparing the nucleotide sequences of the polynucleotides when aligned so as to maximize overlap and identity while minimizing sequence gaps. Allelic variants may be isolated and identified by making suitable probes or primers from the sequences provided  
10 herein and screening a suitable nucleic acid source from individuals of the appropriate species.

The invention also includes polynucleotides with sequences complementary to those of the polynucleotides disclosed herein.

The present invention also includes polynucleotides that hybridize under reduced  
15 stringency conditions, more preferably stringent conditions, and most preferably highly stringent conditions, to polynucleotides described herein. Examples of stringency conditions are shown in the table below: highly stringent conditions are those that are at least as stringent as, for example, conditions A-F; stringent conditions are at least as stringent as, for example, conditions G-L; and reduced stringency conditions are at least as stringent as, for example, conditions M-R.

	Stringency Condition	Polynucleotide Hybrid	Hybrid Length (bp) <sup>†</sup>	Hybridization Temperature and Buffer <sup>†</sup>	Wash Temperature and Buffer <sup>†</sup>
5	A	DNA:DNA	≥ 50	65°C; 1xSSC -or- 42°C; 1xSSC, 50% formamide	65°C; 0.3xSSC
	B	DNA:DNA	<50	T <sub>B</sub> *; 1xSSC	T <sub>B</sub> *; 1xSSC
	C	DNA:RNA	≥ 50	67°C; 1xSSC -or- 45°C; 1xSSC, 50% formamide	67°C; 0.3xSSC
	D	DNA:RNA	<50	T <sub>D</sub> *; 1xSSC	T <sub>D</sub> *; 1xSSC
	E	RNA:RNA	≥ 50	70°C; 1xSSC -or- 50°C; 1xSSC, 50% formamide	70°C; 0.3xSSC
	F	RNA:RNA	<50	T <sub>F</sub> *; 1xSSC	T <sub>F</sub> *; 1xSSC
10	G	DNA:DNA	≥ 50	65°C; 4xSSC -or- 42°C; 4xSSC, 50% formamide	65°C; 1xSSC
	H	DNA:DNA	<50	T <sub>H</sub> *; 4xSSC	T <sub>H</sub> *; 4xSSC
	I	DNA:RNA	≥ 50	67°C; 4xSSC -or- 45°C; 4xSSC, 50% formamide	67°C; 1xSSC
	J	DNA:RNA	<50	T <sub>J</sub> *; 4xSSC	T <sub>J</sub> *; 4xSSC
	K	RNA:RNA	≥ 50	70°C; 4xSSC -or- 50°C; 4xSSC, 50% formamide	67°C; 1xSSC
	L	RNA:RNA	<50	T <sub>L</sub> *; 2xSSC	T <sub>L</sub> *; 2xSSC
15	M	DNA:DNA	≥ 50	50°C; 4xSSC -or- 40°C; 6xSSC, 50% formamide	50°C; 2xSSC
	N	DNA:DNA	<50	T <sub>N</sub> *; 6xSSC	T <sub>N</sub> *; 6xSSC
	O	DNA:RNA	≥ 50	55°C; 4xSSC -or- 42°C; 6xSSC, 50% formamide	55°C; 2xSSC
	P	DNA:RNA	<50	T <sub>P</sub> *; 6xSSC	T <sub>P</sub> *; 6xSSC
	Q	RNA:RNA	≥ 50	60°C; 4xSSC -or- 45°C; 6xSSC, 50% formamide	60°C; 2xSSC
	R	RNA:RNA	<50	T <sub>R</sub> *; 4xSSC	T <sub>R</sub> *; 4xSSC

<sup>†</sup>: The hybrid length is that anticipated for the hybridized region(s) of the hybridizing polynucleotides. When hybridizing a polynucleotide to a target polynucleotide of unknown sequence, the hybrid length is assumed to be that of the hybridizing polynucleotide. When polynucleotides of known sequence are hybridized, the hybrid length can be determined by aligning the sequences of the polynucleotides and identifying the region or regions of optimal sequence complementarity.

<sup>†</sup>: SSPE (1xSSPE is 0.15M NaCl, 10mM NaH<sub>2</sub>PO<sub>4</sub>, and 1.25mM EDTA, pH 7.4) can be substituted for SSC (1xSSC is 0.15M NaCl and 15mM sodium citrate) in the hybridization and wash buffers; washes are performed for 15 minutes after hybridization is complete.

\*T<sub>B</sub> - T<sub>R</sub>: The hybridization temperature for hybrids anticipated to be less than 50 base pairs in length should be 5-10°C less than the melting temperature (T<sub>m</sub>) of the hybrid, where T<sub>m</sub> is determined according to the following equations. For hybrids less than 18 base pairs in length, T<sub>m</sub>(°C) = 2(# of A + T bases) + 4(# of G + C bases). For hybrids between 18 and 49 base pairs in length, T<sub>m</sub>(°C) = 81.5 + 16.6(log<sub>10</sub>[Na<sup>+</sup>]) + 0.41(%G+C) - (600/N), where N is the number of bases in the hybrid, and [Na<sup>+</sup>] is the concentration of sodium ions in the hybridization buffer ([Na<sup>+</sup>] for 1xSSC = 0.165 M).

Additional examples of stringency conditions for polynucleotide hybridization are provided in Sambrook, J., E.F. Fritsch, and T. Maniatis, 1989, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, chapters 9 and 11, and *Current Protocols in Molecular Biology*, 1995, F.M. Ausubel et al., eds., John Wiley & Sons, Inc., sections 2.10 and 6.3-6.4, incorporated herein by reference.

Preferably, each such hybridizing polynucleotide has a length that is at least 25% (more preferably at least 50%, and most preferably at least 75%) of the length of the polynucleotide of the present invention to which it hybridizes, and has at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% or 95% identity) with the polynucleotide of the present invention to which it hybridizes, where sequence identity is determined by comparing the sequences of the hybridizing polynucleotides when aligned so as to maximize overlap and identity while minimizing sequence gaps.

The isolated polynucleotide encoding the protein of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman *et al.*, *Nucleic Acids Res.* 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, *Methods in Enzymology* 185, 537-566 (1990). As defined herein "operably linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

A number of types of cells may act as suitable host cells for expression of the protein. Mammalian host cells include, for example, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3 cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from in vitro culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells.

Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces* strains, *Candida*, or any yeast strain capable of expressing heterologous proteins. Potentially suitable

bacterial strains include *Escherichia coli*, *Bacillus subtilis*, *Salmonella typhimurium*, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, e.g., Invitrogen, San Diego, California, U.S.A. (the MaxBac® kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (i.e., from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearl® or Cibacrom blue 3GA Sepharose®; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX). Kits for expression and purification of such fusion proteins are commercially available from New England BioLabs (Beverly, MA), Pharmacia (Piscataway, NJ) and Invitrogen Corporation (Carlsbad, CA), respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope.



One such epitope ("Flag") is commercially available from the Eastman Kodak Company (New Haven, CT).

Finally, one or more reverse-phase high performance liquid chromatography (RP-HPLC) steps employing hydrophobic RP-HPLC media, e.g., silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The protein of the invention may also be expressed as a product of transgenic animals, e.g., as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

The protein may also be produced by known conventional chemical synthesis. Methods for constructing the proteins of the present invention by synthetic means are known to those skilled in the art. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications in the peptide or DNA sequences can be made by those skilled in the art using known techniques. Modifications of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, e.g., U.S. Patent No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein.

Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and may thus be useful for screening or other immunological methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are believed to be encompassed by the present invention.

## **USES AND BIOLOGICAL ACTIVITY**

The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified below. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or by administration or use of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA).

### **Research Uses and Utilities**

The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on Southern gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, those described in Gyuris *et al.*, 1993, *Cell*

75: 791-803 and in Rossi *et al.*, 1997, *Proc. Natl. Acad. Sci. USA* **94**: 8405-8410, all of which are incorporated by reference herein) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The proteins provided by the present invention can similarly be used in assay to  
5 determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue  
10 differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Where the protein binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the protein can be used to identify the other protein with which binding occurs or to identify inhibitors of the binding interaction. Proteins involved in these binding interactions can also be used to screen for peptide or  
15 small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning:  
20 A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E.F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S.L. and A.R. Kimmel eds., 1987.

#### Nutritional Uses

25 Polynucleotides and proteins of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the protein or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid  
30 preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the protein or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

Cytokine and Cell Proliferation/Differentiation Activity

A protein of the present invention may exhibit cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor-dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+ (preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e and CMK.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for T-cell or thymocyte proliferation include without limitation those described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., *J. Immunol.* 137:3494-3500, 1986; Bertagnolli et al., *J. Immunol.* 145:1706-1712, 1990; Bertagnolli et al., *Cellular Immunology* 133:327-341, 1991; Bertagnolli, et al., *J. Immunol.* 149:3778-3783, 1992; Bowman et al., *J. Immunol.* 152: 1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A.M. and Shevach, E.M. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human Interferon  $\gamma$ , Schreiber, R.D. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L.S. and Lipsky, P.E. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., *J. Exp. Med.* 173:1205-1211, 1991; Moreau et al.,

- Nature 336:690-692, 1988; Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse and human interleukin 6 - Nordan, R. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., Proc. Natl. Acad. Sci. U.S.A. 83:1857-1861, 1986; Measurement of
- 5 human Interleukin 11 - Bennett, F., Giannotti, J., Clark, S.C. and Turner, K. J. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9 - Ciarletta, A., Giannotti, J., Clark, S.C. and Turner, K.J. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.
- 10 Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience
- 15 (Chapter 3, In Vitro assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

20

#### Immune Stimulating or Suppressing Activity

- A protein of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A protein may be useful in the treatment of various immune deficiencies
- 25 and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases caused by viral,
- 30 bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as candidiasis. Of course,

in this regard, a protein of the present invention may also be useful where a boost to the immune system generally may be desirable, *i.e.*, in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitus, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein of the present invention may also be useful in the treatment of allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein of the present invention.

Using the proteins of the invention it may also be possible to regulate immune responses in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as , for example, B7)), *e.g.*, preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble,

monomeric form of a peptide having B7-2 activity alone or in conjunction with a monomeric form of a peptide having an activity of another B lymphocyte antigen (*e.g.*, B7-1, B7-3) or blocking antibody), prior to transplantation can lead to the binding of the molecule to the natural ligand(s) on the immune cells without transmitting the  
5 corresponding costimulatory signal. Blocking B lymphocyte antigen function in this matter prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, the lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated  
10 administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans.  
15 Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins *in vivo* as described in Lenschow *et al.*, Science 257:789-792 (1992) and Turka *et al.*, Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed.,  
20 Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function *in vivo* on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate  
25 activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block costimulation of T cells by disrupting receptor:ligand interactions of B lymphocyte antigens can be used to inhibit T cell  
30 activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the

disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythematosus in MRL/lpr/lpr mice or NZB hybrid mice, murine  
5 autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy.  
10 Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response through stimulating B lymphocyte antigen function may be useful in cases of viral infection. In addition, systemic viral diseases such as influenza, the common cold, and encephalitis might be alleviated by the administration of stimulatory forms of B  
15 lymphocyte antigens systemically.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells *in vitro* with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the *in vitro*  
20 activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory  
25 signal to, and thereby activate, T cells *in vivo*.

In another application, up regulation or enhancement of antigen function (preferably B lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells (*e.g.*, sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least one peptide of the present  
30 invention can be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. For example, tumor cells obtained from a patient can be transfected *ex vivo* with an



expression vector directing the expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The transfected tumor cells are returned to the patient to result in expression of the peptides on the surface of the transfected cell. Alternatively, gene therapy techniques can be used to  
5 target a tumor cell for transfection *in vivo*.

The presence of the peptide of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary costimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II  
10 molecules, or which fail to reexpress sufficient amounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (*e.g.*, a cytoplasmic-domain truncated portion) of an MHC class I  $\alpha$  chain protein and  $\beta_2$  microglobulin protein or an MHC class II  $\alpha$  chain protein and an MHC class II  $\beta$  chain protein to thereby express MHC class I or MHC class II proteins on the cell surface.  
15 Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (*e.g.*, B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the  
20 activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured  
25 by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte  
30 Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol.

137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Bowman et al., J. Virology 61:1992-1998; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: *In vitro* antibody production, Mond, J.J. and Brunswick, M. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, *Immunologic studies in Humans*); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., *Journal of Experimental Medicine* 173:549-559, 1991; Macatonia et al., *Journal of Immunology* 154:5071-5079, 1995; Porgador et al., *Journal of Experimental Medicine* 182:255-260, 1995; Nair et al., *Journal of Virology* 67:4062-4069, 1993; Huang et al., *Science* 264:961-965, 1994; Macatonia et al., *Journal of Experimental Medicine* 169:1255-1264, 1989; Bhardwaj et al., *Journal of Clinical Investigation* 94:797-807, 1994; and Inaba et al., *Journal of Experimental Medicine* 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz

et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

5        Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

#### 10        Hematopoiesis Regulating Activity

A protein of the present invention may be useful in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and  
15 proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for  
20 example, in conjunction with chemotherapy to prevent or treat consequent myelosuppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic  
25 stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either *in-vivo* or *ex-vivo* (i.e., in conjunction  
30 with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

- 5           Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. *Cellular Biology* 15:141-151, 1995; Keller et al., *Molecular and Cellular Biology* 13:473-486, 1993; McClanahan et al., *Blood* 81:2903-2915, 1993.
- 10           Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M.G. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, NY. 1994; Hirayama et al., *Proc. Natl. Acad. Sci. USA* 89:5907-5911, 1992; Primitive hematopoietic
- 15 colony forming cells with high proliferative potential, McNiece, I.K. and Briddell, R.A. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, NY. 1994; Neben et al., *Experimental Hematology* 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R.E. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, NY. 1994; Long term
- 20 bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, NY. 1994; Long term culture initiating cell assay, Sutherland, H.J. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, NY. 1994.

25

#### Tissue Growth Activity

- A protein of the present invention also may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions
- 30 and ulcers.

A protein of the present invention, which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone

fractures and cartilage damage or defects in humans and other animals. Such a preparation employing a protein of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. *De novo* bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A protein of this invention may also be used in the treatment of periodontal disease, and in other tooth repair processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of progenitors of bone-forming cells. A protein of the invention may also be useful in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

Another category of tissue regeneration activity that may be attributable to the protein of the present invention is tendon/ligament formation. A protein of the present invention, which induces tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. *De novo* tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide an environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The protein of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue.

5 More specifically, a protein may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include  
10 mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a protein of the invention.

Proteins of the invention may also be useful to promote better or faster closure of  
15 non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

It is expected that a protein of the present invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac)  
20 and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring to allow normal tissue to regenerate. A protein of the invention may also exhibit angiogenic activity.

A protein of the present invention may also be useful for gut protection or  
25 regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A protein of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

30 The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium ).

- 5        Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, HI and Rovee, DT, eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

10        Activin/Inhibin Activity

- A protein of the present invention may also exhibit activin- or inhibin-related activities. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins and are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a protein of the present
- 15    invention, alone or in heterodimers with a member of the inhibin  $\alpha$  family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin- $\beta$
- 20    group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, United States Patent 4,798,885. A protein of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as cows, sheep and pigs.

- 25        The activity of a protein of the invention may, among other means, be measured by the following methods:

- Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., Endocrinology 91:562-572, 1972; Ling et al., Nature 321:779-782, 1986; Vale et al., Nature 321:776-779, 1986; Mason et al., Nature 318:659-663, 1985; Forage et al.,
- 30    Proc. Natl. Acad. Sci. USA 83:3091-3095, 1986.

Chemotactic/Chemokinetic Activity

A protein of the present invention may have chemotactic or chemokinetic activity (e.g., act as a chemokine) for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. Chemotactic and chemokinetic proteins can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic proteins provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

10 A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25: 1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153: 1762-1768, 1994.

#### Hemostatic and Thrombolytic Activity

30 A protein of the invention may also exhibit hemostatic or thrombolytic activity. As a result, such a protein is expected to be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation



and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A protein of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels  
5 (e.g., stroke).

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis  
10 Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

#### Receptor/Ligand Activity

A protein of the present invention may also demonstrate activity as receptors,  
15 receptor ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs  
20 involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses). Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

25 The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W. Strober, Pub. Greene Publishing Associates and  
30 Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1-7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med.

169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

#### Anti-Inflammatory Activity

5 Proteins of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or  
10 suppressing production of other factors which more directly inhibit or promote an inflammatory response. Proteins exhibiting such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin  
15 lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Proteins of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

#### Cadherin/Tumor Invasion Suppressor Activity

20 Cadherins are calcium-dependent adhesion molecules that appear to play major roles during development, particularly in defining specific cell types. Loss or alteration of normal cadherin expression can lead to changes in cell adhesion properties linked to tumor growth and metastasis. Cadherin malfunction is also implicated in other human diseases, such as pemphigus  
25 vulgaris and pemphigus foliaceus (auto-immune blistering skin diseases), Crohn's disease, and some developmental abnormalities.

The cadherin superfamily includes well over forty members, each with a distinct pattern of expression. All members of the superfamily have in common conserved extracellular repeats (cadherin domains), but structural differences are found in other parts of the molecule. The  
30 cadherin domains bind calcium to form their tertiary structure and thus calcium is required to mediate their adhesion. Only a few amino acids in the first cadherin domain provide the basis for homophilic adhesion; modification of this recognition site can change the specificity of a cadherin

so that instead of recognizing only itself, the mutant molecule can now also bind to a different cadherin. In addition, some cadherins engage in heterophilic adhesion with other cadherins.

E-cadherin, one member of the cadherin superfamily, is expressed in epithelial cell types. Pathologically, if E-cadherin expression is lost in a tumor, the malignant cells become invasive and the cancer metastasizes. Transfection of cancer cell lines with polynucleotides expressing E-cadherin has reversed cancer-associated changes by returning altered cell shapes to normal, restoring cells' adhesiveness to each other and to their substrate, decreasing the cell growth rate, and drastically reducing anchorage-independent cell growth. Thus, reintroducing E-cadherin expression reverts carcinomas to a less advanced stage. It is likely that other cadherins have the same invasion suppressor role in carcinomas derived from other tissue types. Therefore, proteins of the present invention with cadherin activity, and polynucleotides of the present invention encoding such proteins, can be used to treat cancer. Introducing such proteins or polynucleotides into cancer cells can reduce or eliminate the cancerous changes observed in these cells by providing normal cadherin expression.

Cancer cells have also been shown to express cadherins of a different tissue type than their origin, thus allowing these cells to invade and metastasize in a different tissue in the body. Proteins of the present invention with cadherin activity, and polynucleotides of the present invention encoding such proteins, can be substituted in these cells for the inappropriately expressed cadherins, restoring normal cell adhesive properties and reducing or eliminating the tendency of the cells to metastasize.

Additionally, proteins of the present invention with cadherin activity, and polynucleotides of the present invention encoding such proteins, can be used to generate antibodies recognizing and binding to cadherins. Such antibodies can be used to block the adhesion of inappropriately expressed tumor-cell cadherins, preventing the cells from forming a tumor elsewhere. Such an anti-cadherin antibody can also be used as a marker for the grade, pathological type, and prognosis of a cancer, i.e. the more progressed the cancer, the less cadherin expression there will be, and this decrease in cadherin expression can be detected by the use of a cadherin-binding antibody.

Fragments of proteins of the present invention with cadherin activity, preferably a polypeptide comprising a decapeptide of the cadherin recognition site, and polynucleotides of the present invention encoding such protein fragments, can also be used to block cadherin function by binding to cadherins and preventing them from binding in ways that produce undesirable effects. Additionally, fragments of proteins of the present invention with cadherin activity, preferably truncated soluble cadherin fragments which have been found to be stable in the

circulation of cancer patients, and polynucleotides encoding such protein fragments, can be used to disturb proper cell-cell adhesion.

Assays for cadherin adhesive and invasive suppressor activity include, without limitation, those described in: Hortsch et al. J Biol Chem 270 (32): 18809-18817, 1995; Miyaki et al. Oncogene 11: 2547-2552, 1995; Ozawa et al. Cell 63: 1033-1038, 1990.

#### Tumor Inhibition Activity

In addition to the activities described above for immunological treatment or prevention of tumors, a protein of the invention may exhibit other anti-tumor activities.

10 A protein may inhibit tumor growth directly or indirectly (such as, for example, via antibody-dependent cell-mediated cytotoxicity (ADCC)). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor precursor tissue, by inhibiting formation of tissues necessary to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit  
15 tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote tumor growth.

#### Other Activities

A protein of the invention may also exhibit one or more of the following additional  
20 activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution,  
25 change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress,  
30 cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic

lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen  
5 in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

### **ADMINISTRATION AND DOSING**

A protein of the present invention (from whatever source derived, including  
10 without limitation from recombinant and non-recombinant sources) may be used in a pharmaceutical composition when combined with a pharmaceutically acceptable carrier. Such a composition may also contain (in addition to protein and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the  
15 effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF,  
20 thrombopoietin, stem cell factor, and erythropoietin. The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or compliment its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein of the invention, or to minimize side effects. Conversely, protein of the present invention may  
25 be included in formulations of the particular cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent.

A protein of the present invention may be active in multimers (e.g., heterodimers  
30 or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithin, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent No. 4,235,871; U.S. Patent No. 4,501,728; U.S. Patent No. 4,837,028; and U.S. Patent No. 4,737,323, all of which are incorporated herein by reference.

As used herein, the term "therapeutically effective amount" means the total amount of each active component of the pharmaceutical composition or method that is sufficient to show a meaningful patient benefit, i.e., treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, administered alone, the term refers to that ingredient alone. When applied to a combination, the term refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein of the present invention is administered to a mammal having a condition to be treated. Protein of the present invention may be administered in accordance with the method of the invention either alone or in combination  
5 with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co-administered with one or more cytokines, lymphokines or other hematopoietic factors, protein of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the  
10 attending physician will decide on the appropriate sequence of administering protein of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

Administration of protein of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a  
15 variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

When a therapeutically effective amount of protein of the present invention is administered orally, protein of the present invention will be in the form of a tablet, capsule,  
20 powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein of the present invention, and preferably from about 25 to 90% protein of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal  
25 or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein  
30 of the present invention, and preferably from about 1 to 50% protein of the present invention.

When a therapeutically effective amount of protein of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art.

The amount of protein of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein of the present invention with which to treat each individual patient. Initially, the attending physician will administer low doses of protein of the present invention and observe the patient's response. Larger doses of protein of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01  $\mu$ g to about 100 mg (preferably about 0.1mg to about 10 mg, more preferably about 0.1  $\mu$ g to about 1 mg) of protein of the present invention per kg body weight.

The duration of intravenous therapy using the pharmaceutical composition of the present invention will vary, depending on the severity of the disease being treated and the condition and potential idiosyncratic response of each individual patient. It is contemplated that the duration of each application of the protein of the present invention will be in the range of 12 to 24 hours of continuous intravenous administration. Ultimately the attending physician will decide on the appropriate duration of intravenous therapy using the pharmaceutical composition of the present invention.

Protein of the invention may also be used to immunize animals to obtain polyclonal and monoclonal antibodies which specifically react with the protein. As used herein, the



term "antibody" includes without limitation a polyclonal antibody, a monoclonal antibody, a chimeric antibody, a single-chain antibody, a CDR-grafted antibody, a humanized antibody, or fragments thereof which bind to the indicated protein. Such term also includes any other species derived from an antibody or antibody sequence which is capable of binding the indicated protein.

Antibodies to a particular protein can be produced by methods well known to those skilled in the art. For example, monoclonal antibodies can be produced by generation of antibody-producing hybridomas in accordance with known methods (see for example, Goding, 1983, *Monoclonal antibodies: principles and practice*, Academic Press Inc., New York; and Yokoyama, 1992, "Production of Monoclonal Antibodies" in *Current Protocols in Immunology*, Unit 2.5, Greene Publishing Assoc. and John Wiley & Sons). Polyclonal sera and antibodies can be produced by inoculation of a mammalian subject with the relevant protein or fragments thereof in accordance with known methods. Fragments of antibodies, receptors, or other reactive peptides can be produced from the corresponding antibodies by cleavage of and collection of the desired fragments in accordance with known methods (see for example, Goding, *supra*; and Andrew et al., 1992, "Fragmentation of Immunoglobulins" in *Current Protocols in Immunology*, Unit 2.8, Greene Publishing Assoc. and John Wiley & Sons). Chimeric antibodies and single chain antibodies can also be produced in accordance with known recombinant methods (see for example, 5,169,939, 5,194,594, and 5,576,184). Humanized antibodies can also be made from corresponding murine antibodies in accordance with well known methods (see for example, U.S. Patent Nos. 5,530,101, 5,585,089, and 5,693,762). Additionally, human antibodies may be produced in non-human animals such as mice that have been genetically altered to express human antibody molecules (see for example Fishwild *et al.*, 1996, *Nature Biotechnology* 14: 845-851; Mendez *et al.*, 1997, *Nature Genetics* 15: 146-156 (erratum *Nature Genetics* 16: 410); and U.S. Patents 5,877,397 and 5,625,126). Such antibodies may be obtained using either the entire protein or fragments thereof as an immunogen. The peptide immunogens additionally may contain a cysteine residue at the carboxyl terminus, and are conjugated to a hapten such as keyhole limpet hemocyanin (KLH). Methods for synthesizing such peptides are known in the art, for example, as in R.P. Merrifield, J. Amer.Chem.Soc. 85, 2149-2154 (1963); J.L. Krstenansky, *et al.*, *FEBS Lett.* 211, 10 (1987).

Monoclonal antibodies binding to the protein of the invention may be useful diagnostic agents for the immunodetection of the protein. Neutralizing monoclonal antibodies binding to the protein may also be useful therapeutics for both conditions associated with the protein and also in the treatment of some forms of cancer where  
5 abnormal expression of the protein is involved. In the case of cancerous cells or leukemic cells, neutralizing monoclonal antibodies against the protein may be useful in detecting and preventing the metastatic spread of the cancerous cells, which may be mediated by the protein.

For compositions of the present invention which are useful for bone, cartilage,  
10 tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systemically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or  
15 tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the invention. Preferably for bone and/or cartilage formation, the composition  
20 would include a matrix capable of delivering the protein-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

The choice of matrix material is based on biocompatibility, biodegradability,  
25 mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices for the compositions may be biodegradable and chemically defined calcium sulfate, tricalciumphosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined,  
30 such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxapatite, bioglass, aluminates, or other ceramics.

Matrices may be comprised of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalciumphosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability.

5        Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

10        A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic  
15 acid, sodium alginate, poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt%, preferably 1-10 wt% based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are  
20 prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells.

In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor  
25 (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF- $\alpha$  and TGF- $\beta$ ), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to humans, are desired patients for such treatment with proteins of the present invention.

30        The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, e.g., amount of tissue weight desired to be

formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (e.g., bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either *in vivo* or *ex vivo* into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA).

Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes.

Patent and literature references cited herein are incorporated by reference as if fully set forth.

What is claimed is:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:1;
- (b) the nucleotide sequence of SEQ ID NO:1 from nucleotide 27 to nucleotide 260;
- (c) the nucleotide sequence of SEQ ID NO:1 from nucleotide 72 to nucleotide 260;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vc62\_1 deposited with the ATCC under accession number 207114;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vc62\_1 deposited with the ATCC under accession number 207114;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vc62\_1 deposited with the ATCC under accession number 207114;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vc62\_1 deposited with the ATCC under accession number 207114;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:2;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2, the fragment comprising eight contiguous amino acids of SEQ ID NO:2;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:1.

2. The polynucleotide of claim 1 wherein said polynucleotide is operably linked to at least one expression control sequence.
3. A host cell transformed with the polynucleotide of claim 2.
4. The host cell of claim 3, wherein said cell is a mammalian cell.
5. A process for producing a protein encoded by the polynucleotide of claim 2, which process comprises:
  - (a) growing a culture of a host cell in a suitable culture medium, wherein the host cell has been transformed with the polynucleotide of claim 2; and
  - (b) purifying said protein from the culture.
6. A protein produced according to the process of claim 5.
7. An isolated polynucleotide encoding the protein of claim 6.
8. The polynucleotide of claim 7, wherein the polynucleotide comprises the cDNA insert of clone vc62\_1 deposited with the ATCC under accession number 207114.
9. A protein comprising an amino acid sequence selected from the group consisting of:
  - (a) the amino acid sequence of SEQ ID NO:2;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:2, the fragment comprising eight contiguous amino acids of SEQ ID NO:2; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone vc62\_1 deposited with the ATCC under accession number 207114;the protein being substantially free from other mammalian proteins.
10. The protein of claim 9, wherein said protein comprises the amino acid sequence of SEQ ID NO:2.

11. A composition comprising the protein of claim 9 and a pharmaceutically acceptable carrier.

12. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:3;
- (b) the nucleotide sequence of SEQ ID NO:3 from nucleotide 6 to nucleotide 1325;
- (c) the nucleotide sequence of SEQ ID NO:3 from nucleotide 99 to nucleotide 1325;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vp10\_1 deposited with the ATCC under accession number 207114;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vp10\_1 deposited with the ATCC under accession number 207114;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vp10\_1 deposited with the ATCC under accession number 207114;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vp10\_1 deposited with the ATCC under accession number 207114;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:4;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4, the fragment comprising eight contiguous amino acids of SEQ ID NO:4;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:3.

13. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:4;
- (b) a fragment of the amino acid sequence of SEQ ID NO:4, the fragment comprising eight contiguous amino acids of SEQ ID NO:4; and
- (c) the amino acid sequence encoded by the cDNA insert of clone vp10\_1 deposited with the ATCC under accession number 207114;

the protein being substantially free from other mammalian proteins.

14. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:5;
- (b) the nucleotide sequence of SEQ ID NO:5 from nucleotide 149 to nucleotide 322;
- (c) the nucleotide sequence of SEQ ID NO:5 from nucleotide 200 to nucleotide 322;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vp11\_1 deposited with the ATCC under accession number 207114;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vp11\_1 deposited with the ATCC under accession number 207114;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vp11\_1 deposited with the ATCC under accession number 207114;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vp11\_1 deposited with the ATCC under accession number 207114;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:6;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6, the fragment comprising eight contiguous amino acids of SEQ ID NO:6;



(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:5.

15. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:6;

(b) a fragment of the amino acid sequence of SEQ ID NO:6, the fragment comprising eight contiguous amino acids of SEQ ID NO:6; and

(c) the amino acid sequence encoded by the cDNA insert of clone vp11\_1 deposited with the ATCC under accession number 207114;

the protein being substantially free from other mammalian proteins.

16. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:7;

(b) the nucleotide sequence of SEQ ID NO:7 from nucleotide 288 to nucleotide 629;

(c) the nucleotide sequence of SEQ ID NO:7 from nucleotide 363 to nucleotide 629;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vp13\_1 deposited with the ATCC under accession number 207114;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vp13\_1 deposited with the ATCC under accession number 207114;

(f) the nucleotide sequence of a mature protein coding sequence of clone vp13\_1 deposited with the ATCC under accession number 207114;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vp13\_1 deposited with the ATCC under accession number 207114;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:8;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8, the fragment comprising eight contiguous amino acids of SEQ ID NO:8;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:7.

17. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:8;

(b) a fragment of the amino acid sequence of SEQ ID NO:8, the fragment comprising eight contiguous amino acids of SEQ ID NO:8; and

(c) the amino acid sequence encoded by the cDNA insert of clone vp13\_1 deposited with the ATCC under accession number 207114;

the protein being substantially free from other mammalian proteins.

18. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:9;

(b) the nucleotide sequence of SEQ ID NO:9 from nucleotide 11 to nucleotide 298;

(c) the nucleotide sequence of SEQ ID NO:9 from nucleotide 149 to nucleotide 298;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vp16\_1 deposited with the ATCC under accession number 207114;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vp16\_1 deposited with the ATCC under accession number 207114;

(f) the nucleotide sequence of a mature protein coding sequence of clone vp16\_1 deposited with the ATCC under accession number 207114;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vp16\_1 deposited with the ATCC under accession number 207114;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:10;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10, the fragment comprising eight contiguous amino acids of SEQ ID NO:10;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:9.

19. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:10;

(b) a fragment of the amino acid sequence of SEQ ID NO:10, the fragment comprising eight contiguous amino acids of SEQ ID NO:10; and

(c) the amino acid sequence encoded by the cDNA insert of clone vp16\_1 deposited with the ATCC under accession number 207114;

the protein being substantially free from other mammalian proteins.

20. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:11;
- (b) the nucleotide sequence of SEQ ID NO:11 from nucleotide 257 to nucleotide 607;
- (c) the nucleotide sequence of SEQ ID NO:11 from nucleotide 479 to nucleotide 607;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vp21\_1 deposited with the ATCC under accession number 207114;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vp21\_1 deposited with the ATCC under accession number 207114;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vp21\_1 deposited with the ATCC under accession number 207114;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vp21\_1 deposited with the ATCC under accession number 207114;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:12;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12, the fragment comprising eight contiguous amino acids of SEQ ID NO:12;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:11.

21. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:12;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:12, the fragment comprising eight contiguous amino acids of SEQ ID NO:12; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone vp21\_1 deposited with the ATCC under accession number 207114;
- the protein being substantially free from other mammalian proteins.

22. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:13;
- (b) the nucleotide sequence of SEQ ID NO:13 from nucleotide 163 to nucleotide 477;
- (c) the nucleotide sequence of SEQ ID NO:13 from nucleotide 238 to nucleotide 477;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vp22\_1 deposited with the ATCC under accession number 207114;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vp22\_1 deposited with the ATCC under accession number 207114;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vp22\_1 deposited with the ATCC under accession number 207114;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vp22\_1 deposited with the ATCC under accession number 207114;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:14;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14, the fragment comprising eight contiguous amino acids of SEQ ID NO:14;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:13.

23. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:14;
- (b) a fragment of the amino acid sequence of SEQ ID NO:14, the fragment comprising eight contiguous amino acids of SEQ ID NO:14; and
- (c) the amino acid sequence encoded by the cDNA insert of clone vp22\_1 deposited with the ATCC under accession number 207114;

the protein being substantially free from other mammalian proteins.

24. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:15;
- (b) the nucleotide sequence of SEQ ID NO:15 from nucleotide 58 to nucleotide 624;
- (c) the nucleotide sequence of SEQ ID NO:15 from nucleotide 106 to nucleotide 624;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vq2\_1 deposited with the ATCC under accession number 207114;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vq2\_1 deposited with the ATCC under accession number 207114;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vq2\_1 deposited with the ATCC under accession number 207114;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vq2\_1 deposited with the ATCC under accession number 207114;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:16;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16, the fragment comprising eight contiguous amino acids of SEQ ID NO:16;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:15.

25. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:16;

(b) a fragment of the amino acid sequence of SEQ ID NO:16, the fragment comprising eight contiguous amino acids of SEQ ID NO:16; and

(c) the amino acid sequence encoded by the cDNA insert of clone vq2\_1 deposited with the ATCC under accession number 207114;

the protein being substantially free from other mammalian proteins.

26. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:17;

(b) the nucleotide sequence of SEQ ID NO:17 from nucleotide 773 to nucleotide 1090;

(c) the nucleotide sequence of SEQ ID NO:17 from nucleotide 842 to nucleotide 1090;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vq3\_1 deposited with the ATCC under accession number 207114;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vq3\_1 deposited with the ATCC under accession number 207114;

(f) the nucleotide sequence of a mature protein coding sequence of clone vq3\_1 deposited with the ATCC under accession number 207114;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vq3\_1 deposited with the ATCC under accession number 207114;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:18;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18, the fragment comprising eight contiguous amino acids of SEQ ID NO:18;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:17.

27. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:18;

(b) a fragment of the amino acid sequence of SEQ ID NO:18, the fragment comprising eight contiguous amino acids of SEQ ID NO:18; and

(c) the amino acid sequence encoded by the cDNA insert of clone vq3\_1 deposited with the ATCC under accession number 207114;

the protein being substantially free from other mammalian proteins.

28. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:



- (a) the nucleotide sequence of SEQ ID NO:19;
- (b) the nucleotide sequence of SEQ ID NO:19 from nucleotide 96 to nucleotide 275;
- (c) the nucleotide sequence of SEQ ID NO:19 from nucleotide 159 to nucleotide 275;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vq5\_1 deposited with the ATCC under accession number 207114;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vq5\_1 deposited with the ATCC under accession number 207114;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vq5\_1 deposited with the ATCC under accession number 207114;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vq5\_1 deposited with the ATCC under accession number 207114;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:20;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20, the fragment comprising eight contiguous amino acids of SEQ ID NO:20;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:19.

29. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:20;

- (b) a fragment of the amino acid sequence of SEQ ID NO:20, the fragment comprising eight contiguous amino acids of SEQ ID NO:20; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone vq5\_1 deposited with the ATCC under accession number 207114;
- the protein being substantially free from other mammalian proteins.

30. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:21;
- (b) the nucleotide sequence of SEQ ID NO:21 from nucleotide 176 to nucleotide 340;
- (c) the nucleotide sequence of SEQ ID NO:21 from nucleotide 230 to nucleotide 340;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vq6\_1 deposited with the ATCC under accession number 207114;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vq6\_1 deposited with the ATCC under accession number 207114;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vq6\_1 deposited with the ATCC under accession number 207114;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vq6\_1 deposited with the ATCC under accession number 207114;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:22;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22, the fragment comprising eight contiguous amino acids of SEQ ID NO:22;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:21.

31. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:22;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:22, the fragment comprising eight contiguous amino acids of SEQ ID NO:22; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone vq6\_1 deposited with the ATCC under accession number 207114;
- the protein being substantially free from other mammalian proteins.

32. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:23;
- (b) the nucleotide sequence of SEQ ID NO:23 from nucleotide 29 to nucleotide 1111;
- (c) the nucleotide sequence of SEQ ID NO:23 from nucleotide 167 to nucleotide 1111;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vr1\_1 deposited with the ATCC under accession number 207114;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vr1\_1 deposited with the ATCC under accession number 207114;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vr1\_1 deposited with the ATCC under accession number 207114;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vr1\_1 deposited with the ATCC under accession number 207114;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:24;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24, the fragment comprising eight contiguous amino acids of SEQ ID NO:24;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:23.

33. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:24;

(b) a fragment of the amino acid sequence of SEQ ID NO:24, the fragment comprising eight contiguous amino acids of SEQ ID NO:24; and

(c) the amino acid sequence encoded by the cDNA insert of clone vr1\_1 deposited with the ATCC under accession number 207114;

the protein being substantially free from other mammalian proteins.

34. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:25;

(b) the nucleotide sequence of SEQ ID NO:25 from nucleotide 13 to nucleotide 513;

(c) the nucleotide sequence of the full-length protein coding sequence of clone vc63\_1 deposited with the ATCC under accession number 207115;

(d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vc63\_1 deposited with the ATCC under accession number 207115;

(e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:26;

(f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26, the fragment comprising eight contiguous amino acids of SEQ ID NO:26;

(g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and

(h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:25.

35. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:26;

(b) a fragment of the amino acid sequence of SEQ ID NO:26, the fragment comprising eight contiguous amino acids of SEQ ID NO:26; and

(c) the amino acid sequence encoded by the cDNA insert of clone vc63\_1 deposited with the ATCC under accession number 207115;

the protein being substantially free from other mammalian proteins.

36. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:27;

(b) the nucleotide sequence of SEQ ID NO:27 from nucleotide 79 to nucleotide 345;

(c) the nucleotide sequence of SEQ ID NO:27 from nucleotide 130 to nucleotide 345;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vb25\_1 deposited with the ATCC under accession number PTA-362;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vb25\_1 deposited with the ATCC under accession number PTA-362;

(f) the nucleotide sequence of a mature protein coding sequence of clone vb25\_1 deposited with the ATCC under accession number PTA-362;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vb25\_1 deposited with the ATCC under accession number PTA-362;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:28;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28, the fragment comprising eight contiguous amino acids of SEQ ID NO:28;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:27.

37. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:28;

(b) a fragment of the amino acid sequence of SEQ ID NO:28, the fragment comprising eight contiguous amino acids of SEQ ID NO:28; and

(c) the amino acid sequence encoded by the cDNA insert of clone vb25\_1 deposited with the ATCC under accession number PTA-362;

the protein being substantially free from other mammalian proteins.

38. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:29;
- (b) the nucleotide sequence of SEQ ID NO:29 from nucleotide 72 to nucleotide 236;
- (c) the nucleotide sequence of SEQ ID NO:29 from nucleotide 150 to nucleotide 236;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vb27\_1 deposited with the ATCC under accession number PTA-362;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vb27\_1 deposited with the ATCC under accession number PTA-362;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vb27\_1 deposited with the ATCC under accession number PTA-362;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vb27\_1 deposited with the ATCC under accession number PTA-362;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:30;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30, the fragment comprising eight contiguous amino acids of SEQ ID NO:30;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:29.

39. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:30;

- (b) a fragment of the amino acid sequence of SEQ ID NO:30, the fragment comprising eight contiguous amino acids of SEQ ID NO:30; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone vb27\_1 deposited with the ATCC under accession number PTA-362;
- the protein being substantially free from other mammalian proteins.

40. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:31;
- (b) the nucleotide sequence of SEQ ID NO:31 from nucleotide 135 to nucleotide 884;
- (c) the nucleotide sequence of SEQ ID NO:31 from nucleotide 183 to nucleotide 884;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vb28\_1 deposited with the ATCC under accession number PTA-362;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vb28\_1 deposited with the ATCC under accession number PTA-362;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vb28\_1 deposited with the ATCC under accession number PTA-362;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vb28\_1 deposited with the ATCC under accession number PTA-362;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:32;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32, the fragment comprising eight contiguous amino acids of SEQ ID NO:32;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and



(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:31.

41. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:32;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:32, the fragment comprising eight contiguous amino acids of SEQ ID NO:32; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone vb28\_1 deposited with the ATCC under accession number PTA-362;
- the protein being substantially free from other mammalian proteins.

42. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:33;
- (b) the nucleotide sequence of SEQ ID NO:33 from nucleotide 42 to nucleotide 206;
- (c) the nucleotide sequence of SEQ ID NO:33 from nucleotide 111 to nucleotide 206;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vb29\_1 deposited with the ATCC under accession number PTA-362;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vb29\_1 deposited with the ATCC under accession number PTA-362;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vb29\_1 deposited with the ATCC under accession number PTA-362;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vb29\_1 deposited with the ATCC under accession number PTA-362;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:34;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34, the fragment comprising eight contiguous amino acids of SEQ ID NO:34;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:33.

43. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:34;

(b) a fragment of the amino acid sequence of SEQ ID NO:34, the fragment comprising eight contiguous amino acids of SEQ ID NO:34; and

(c) the amino acid sequence encoded by the cDNA insert of clone vb29\_1 deposited with the ATCC under accession number PTA-362;

the protein being substantially free from other mammalian proteins.

44. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:35;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:35 from nucleotide 17 to nucleotide 253;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:35 from nucleotide 98 to nucleotide 253;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vb30\_1 deposited with the ATCC under accession number PTA-362;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vb30\_1 deposited with the ATCC under accession number PTA-362;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vb30\_1 deposited with the ATCC under accession number PTA-362;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vb30\_1 deposited with the ATCC under accession number PTA-362;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:36;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:36;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:35.

45. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:36;

(b) a fragment of the amino acid sequence of SEQ ID NO:36, the fragment comprising eight contiguous amino acids of SEQ ID NO:36; and

(c) the amino acid sequence encoded by the cDNA insert of clone vb30\_1 deposited with the ATCC under accession number PTA-362; the protein being substantially free from other mammalian proteins.

46. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:37;
- (b) the nucleotide sequence of SEQ ID NO:37 from nucleotide 68 to nucleotide 424;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone vc67\_1 deposited with the ATCC under accession number PTA-362;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vc67\_1 deposited with the ATCC under accession number PTA-362;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:38;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38, the fragment comprising eight contiguous amino acids of SEQ ID NO:38;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:37.

47. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:38;
- (b) a fragment of the amino acid sequence of SEQ ID NO:38, the fragment comprising eight contiguous amino acids of SEQ ID NO:38; and

(c) the amino acid sequence encoded by the cDNA insert of clone vc67\_1 deposited with the ATCC under accession number PTA-362; the protein being substantially free from other mammalian proteins.

48. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:39;
- (b) the nucleotide sequence of SEQ ID NO:39 from nucleotide 103 to nucleotide 261;
- (c) the nucleotide sequence of SEQ ID NO:39 from nucleotide 154 to nucleotide 261;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vf4\_1 deposited with the ATCC under accession number PTA-362;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vf4\_1 deposited with the ATCC under accession number PTA-362;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vf4\_1 deposited with the ATCC under accession number PTA-362;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vf4\_1 deposited with the ATCC under accession number PTA-362;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:40;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40, the fragment comprising eight contiguous amino acids of SEQ ID NO:40;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees

C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:39.

49. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:40;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:40, the fragment comprising eight contiguous amino acids of SEQ ID NO:40; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone vf4\_1 deposited with the ATCC under accession number PTA-362;
- the protein being substantially free from other mammalian proteins.

50. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:41;
- (b) the nucleotide sequence of SEQ ID NO:41 from nucleotide 1575 to nucleotide 3038;
- (c) the nucleotide sequence of SEQ ID NO:41 from nucleotide 1650 to nucleotide 3038;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vg3\_1 deposited with the ATCC under accession number PTA-362;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vg3\_1 deposited with the ATCC under accession number PTA-362;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vg3\_1 deposited with the ATCC under accession number PTA-362;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vg3\_1 deposited with the ATCC under accession number PTA-362;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:42;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42, the fragment comprising eight contiguous amino acids of SEQ ID NO:42;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:41.

51. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:42;

(b) a fragment of the amino acid sequence of SEQ ID NO:42, the fragment comprising eight contiguous amino acids of SEQ ID NO:42; and

(c) the amino acid sequence encoded by the cDNA insert of clone vg3\_1 deposited with the ATCC under accession number PTA-362;

the protein being substantially free from other mammalian proteins.

52. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:43;

(b) the nucleotide sequence of SEQ ID NO:43 from nucleotide 2112 to nucleotide 2363;

(c) the nucleotide sequence of the full-length protein coding sequence of clone vo2\_1 deposited with the ATCC under accession number PTA-362;

(d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo2\_1 deposited with the ATCC under accession number PTA-362;

(e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:44;

(f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44, the fragment comprising eight contiguous amino acids of SEQ ID NO:44;

(g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and

(h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:43.

53. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:44;

(b) a fragment of the amino acid sequence of SEQ ID NO:44, the fragment comprising eight contiguous amino acids of SEQ ID NO:44; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo2\_1 deposited with the ATCC under accession number PTA-362;

the protein being substantially free from other mammalian proteins.

54. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:45;

(b) the nucleotide sequence of SEQ ID NO:45 from nucleotide 36 to nucleotide 707;

(c) the nucleotide sequence of SEQ ID NO:45 from nucleotide 393 to nucleotide 707;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vo3\_1 deposited with the ATCC under accession number PTA-362;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo3\_1 deposited with the ATCC under accession number PTA-362;



- (f) the nucleotide sequence of a mature protein coding sequence of clone vo3\_1 deposited with the ATCC under accession number PTA-362;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vo3\_1 deposited with the ATCC under accession number PTA-362;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:46;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:46, the fragment comprising eight contiguous amino acids of SEQ ID NO:46;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:45.

55. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:46;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:46, the fragment comprising eight contiguous amino acids of SEQ ID NO:46; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone vo3\_1 deposited with the ATCC under accession number PTA-362;
- the protein being substantially free from other mammalian proteins.

56. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:47;
- (b) the nucleotide sequence of SEQ ID NO:47 from nucleotide 74 to nucleotide 295;

- (c) the nucleotide sequence of SEQ ID NO:47 from nucleotide 134 to nucleotide 295;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vo5\_1 deposited with the ATCC under accession number PTA-362;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo5\_1 deposited with the ATCC under accession number PTA-362;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vo5\_1 deposited with the ATCC under accession number PTA-362;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vo5\_1 deposited with the ATCC under accession number PTA-362;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:48;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48, the fragment comprising eight contiguous amino acids of SEQ ID NO:48;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:47.

57. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:48;
- (b) a fragment of the amino acid sequence of SEQ ID NO:48, the fragment comprising eight contiguous amino acids of SEQ ID NO:48; and
- (c) the amino acid sequence encoded by the cDNA insert of clone vo5\_1 deposited with the ATCC under accession number PTA-362;

the protein being substantially free from other mammalian proteins.

58. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:49;
- (b) the nucleotide sequence of SEQ ID NO:49 from nucleotide 45 to nucleotide 383;
- (c) the nucleotide sequence of SEQ ID NO:49 from nucleotide 312 to nucleotide 383;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vo6\_1 deposited with the ATCC under accession number PTA-362;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo6\_1 deposited with the ATCC under accession number PTA-362;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vo6\_1 deposited with the ATCC under accession number PTA-362;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vo6\_1 deposited with the ATCC under accession number PTA-362;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:50;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50, the fragment comprising eight contiguous amino acids of SEQ ID NO:50;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:49.

59. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:50;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:50, the fragment comprising eight contiguous amino acids of SEQ ID NO:50; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone vo6\_1 deposited with the ATCC under accession number PTA-362;
- the protein being substantially free from other mammalian proteins.

60. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:51;
- (b) the nucleotide sequence of SEQ ID NO:51 from nucleotide 186 to nucleotide 1739;
- (c) the nucleotide sequence of SEQ ID NO:51 from nucleotide 288 to nucleotide 1739;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vo9\_1 deposited with the ATCC under accession number PTA-362;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo9\_1 deposited with the ATCC under accession number PTA-362;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vo9\_1 deposited with the ATCC under accession number PTA-362;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vo9\_1 deposited with the ATCC under accession number PTA-362;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:52;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52, the fragment comprising eight contiguous amino acids of SEQ ID NO:52;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:51.

61. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:52;

(b) a fragment of the amino acid sequence of SEQ ID NO:52, the fragment comprising eight contiguous amino acids of SEQ ID NO:52; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo9\_1 deposited with the ATCC under accession number PTA-362;

the protein being substantially free from other mammalian proteins.

62. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:53;

(b) the nucleotide sequence of SEQ ID NO:53 from nucleotide 440 to nucleotide 835;

(c) the nucleotide sequence of SEQ ID NO:53 from nucleotide 632 to nucleotide 835;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vo11\_1 deposited with the ATCC under accession number PTA-366;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo11\_1 deposited with the ATCC under accession number PTA-366;

(f) the nucleotide sequence of a mature protein coding sequence of clone vo11\_1 deposited with the ATCC under accession number PTA-366;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vo11\_1 deposited with the ATCC under accession number PTA-366;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:54;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54, the fragment comprising eight contiguous amino acids of SEQ ID NO:54;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:53.

63. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:54;

(b) a fragment of the amino acid sequence of SEQ ID NO:54, the fragment comprising eight contiguous amino acids of SEQ ID NO:54; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo11\_1 deposited with the ATCC under accession number PTA-366;

the protein being substantially free from other mammalian proteins.

64. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:55;

(b) the nucleotide sequence of SEQ ID NO:55 from nucleotide 72 to nucleotide 329;

(c) the nucleotide sequence of SEQ ID NO:55 from nucleotide 120 to nucleotide 329;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vo12\_1 deposited with the ATCC under accession number PTA-366;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo12\_1 deposited with the ATCC under accession number PTA-366;

(f) the nucleotide sequence of a mature protein coding sequence of clone vo12\_1 deposited with the ATCC under accession number PTA-366;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vo12\_1 deposited with the ATCC under accession number PTA-366;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:56;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56, the fragment comprising eight contiguous amino acids of SEQ ID NO:56;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:55.

65. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:56;

(b) a fragment of the amino acid sequence of SEQ ID NO:56, the fragment comprising eight contiguous amino acids of SEQ ID NO:56; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo12\_1 deposited with the ATCC under accession number PTA-366;

the protein being substantially free from other mammalian proteins.

66. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:57;
- (b) the nucleotide sequence of SEQ ID NO:57 from nucleotide 227 to nucleotide 439;
- (c) the nucleotide sequence of SEQ ID NO:57 from nucleotide 287 to nucleotide 439;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vo13\_1 deposited with the ATCC under accession number PTA-366;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo13\_1 deposited with the ATCC under accession number PTA-366;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vo13\_1 deposited with the ATCC under accession number PTA-366;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vo13\_1 deposited with the ATCC under accession number PTA-366;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:58;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58, the fragment comprising eight contiguous amino acids of SEQ ID NO:58;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:57.

67. A protein comprising an amino acid sequence selected from the group consisting of:



- (a) the amino acid sequence of SEQ ID NO:58;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:58, the fragment comprising eight contiguous amino acids of SEQ ID NO:58; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone vo13\_1 deposited with the ATCC under accession number PTA-366;
- the protein being substantially free from other mammalian proteins.

68. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:59;
- (b) the nucleotide sequence of SEQ ID NO:59 from nucleotide 96 to nucleotide 341;
- (c) the nucleotide sequence of SEQ ID NO:59 from nucleotide 174 to nucleotide 341;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vo14\_1 deposited with the ATCC under accession number PTA-366;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo14\_1 deposited with the ATCC under accession number PTA-366;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vo14\_1 deposited with the ATCC under accession number PTA-366;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vo14\_1 deposited with the ATCC under accession number PTA-366;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:60;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60, the fragment comprising eight contiguous amino acids of SEQ ID NO:60;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:59.

69. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:60;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:60, the fragment comprising eight contiguous amino acids of SEQ ID NO:60; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone vo14\_1 deposited with the ATCC under accession number PTA-366;
- the protein being substantially free from other mammalian proteins.

70. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:61;
- (b) the nucleotide sequence of SEQ ID NO:61 from nucleotide 90 to nucleotide 599;
- (c) the nucleotide sequence of SEQ ID NO:61 from nucleotide 165 to nucleotide 599;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vo15\_1 deposited with the ATCC under accession number PTA-366;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo15\_1 deposited with the ATCC under accession number PTA-366;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vo15\_1 deposited with the ATCC under accession number PTA-366;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vo15\_1 deposited with the ATCC under accession number PTA-366;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:62;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62, the fragment comprising eight contiguous amino acids of SEQ ID NO:62;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:61.

71. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:62;

(b) a fragment of the amino acid sequence of SEQ ID NO:62, the fragment comprising eight contiguous amino acids of SEQ ID NO:62; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo15\_1 deposited with the ATCC under accession number PTA-366;

the protein being substantially free from other mammalian proteins.

72. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:63;

(b) the nucleotide sequence of SEQ ID NO:63 from nucleotide 209 to nucleotide 451;

(c) the nucleotide sequence of SEQ ID NO:63 from nucleotide 398 to nucleotide 451;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vo16\_1 deposited with the ATCC under accession number PTA-366;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo16\_1 deposited with the ATCC under accession number PTA-366;

(f) the nucleotide sequence of a mature protein coding sequence of clone vo16\_1 deposited with the ATCC under accession number PTA-366;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vo16\_1 deposited with the ATCC under accession number PTA-366;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:64;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64, the fragment comprising eight contiguous amino acids of SEQ ID NO:64;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:63.

73. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:64;

(b) a fragment of the amino acid sequence of SEQ ID NO:64, the fragment comprising eight contiguous amino acids of SEQ ID NO:64; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo16\_1 deposited with the ATCC under accession number PTA-366;

the protein being substantially free from other mammalian proteins.

74. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:65;
- (b) the nucleotide sequence of SEQ ID NO:65 from nucleotide 31 to nucleotide 231;
- (c) the nucleotide sequence of SEQ ID NO:65 from nucleotide 97 to nucleotide 231;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vo18\_1 deposited with the ATCC under accession number PTA-366;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo18\_1 deposited with the ATCC under accession number PTA-366;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vo18\_1 deposited with the ATCC under accession number PTA-366;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vo18\_1 deposited with the ATCC under accession number PTA-366;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:66;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:66, the fragment comprising eight contiguous amino acids of SEQ ID NO:66;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:65.

75. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:66;

- (b) a fragment of the amino acid sequence of SEQ ID NO:66, the fragment comprising eight contiguous amino acids of SEQ ID NO:66; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone vo18\_1 deposited with the ATCC under accession number PTA-366;
- the protein being substantially free from other mammalian proteins.

76. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:67;
- (b) the nucleotide sequence of SEQ ID NO:67 from nucleotide 23 to nucleotide 736;
- (c) the nucleotide sequence of SEQ ID NO:67 from nucleotide 83 to nucleotide 736;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vo19\_1 deposited with the ATCC under accession number PTA-366;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo19\_1 deposited with the ATCC under accession number PTA-366;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vo19\_1 deposited with the ATCC under accession number PTA-366;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vo19\_1 deposited with the ATCC under accession number PTA-366;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:68;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:68, the fragment comprising eight contiguous amino acids of SEQ ID NO:68;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:67.

77. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:68;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:68, the fragment comprising eight contiguous amino acids of SEQ ID NO:68; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone vo19\_1 deposited with the ATCC under accession number PTA-366;
- the protein being substantially free from other mammalian proteins.

78. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:69;
- (b) the nucleotide sequence of SEQ ID NO:69 from nucleotide 104 to nucleotide 1399;
- (c) the nucleotide sequence of SEQ ID NO:69 from nucleotide 158 to nucleotide 1399;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vo22\_1 deposited with the ATCC under accession number PTA-366;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo22\_1 deposited with the ATCC under accession number PTA-366;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vo22\_1 deposited with the ATCC under accession number PTA-366;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vo22\_1 deposited with the ATCC under accession number PTA-366;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:70;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:70, the fragment comprising eight contiguous amino acids of SEQ ID NO:70;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:69.

79. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:70;

(b) a fragment of the amino acid sequence of SEQ ID NO:70, the fragment comprising eight contiguous amino acids of SEQ ID NO:70; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo22\_1 deposited with the ATCC under accession number PTA-366;

the protein being substantially free from other mammalian proteins.

80. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:71;

(b) the nucleotide sequence of SEQ ID NO:71 from nucleotide 174 to nucleotide 1595;

(c) the nucleotide sequence of the full-length protein coding sequence of clone vo23\_1 deposited with the ATCC under accession number PTA-366;

(d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo23\_1 deposited with the ATCC under accession number PTA-366;



(e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:72;

(f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:72, the fragment comprising eight contiguous amino acids of SEQ ID NO:72;

(g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and

(h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:71.

81. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:72;

(b) a fragment of the amino acid sequence of SEQ ID NO:72, the fragment comprising eight contiguous amino acids of SEQ ID NO:72; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo23\_1 deposited with the ATCC under accession number PTA-366;

the protein being substantially free from other mammalian proteins.

82. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:73;

(b) the nucleotide sequence of SEQ ID NO:73 from nucleotide 129 to nucleotide 311;

(c) the nucleotide sequence of SEQ ID NO:73 from nucleotide 195 to nucleotide 311;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vo24\_1 deposited with the ATCC under accession number PTA-366;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo24\_1 deposited with the ATCC under accession number PTA-366;

(f) the nucleotide sequence of a mature protein coding sequence of clone vo24\_1 deposited with the ATCC under accession number PTA-366;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vo24\_1 deposited with the ATCC under accession number PTA-366;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:74;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:74, the fragment comprising eight contiguous amino acids of SEQ ID NO:74;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:73.

83. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:74;

(b) a fragment of the amino acid sequence of SEQ ID NO:74, the fragment comprising eight contiguous amino acids of SEQ ID NO:74; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo24\_1 deposited with the ATCC under accession number PTA-366;

the protein being substantially free from other mammalian proteins.

84. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:75;
- (b) the nucleotide sequence of SEQ ID NO:75 from nucleotide 73 to nucleotide 798;
- (c) the nucleotide sequence of SEQ ID NO:75 from nucleotide 142 to nucleotide 798;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vo25\_1 deposited with the ATCC under accession number PTA-366;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo25\_1 deposited with the ATCC under accession number PTA-366;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vo25\_1 deposited with the ATCC under accession number PTA-366;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vo25\_1 deposited with the ATCC under accession number PTA-366;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:76;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76, the fragment comprising eight contiguous amino acids of SEQ ID NO:76;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:75.

85. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:76;

(b) a fragment of the amino acid sequence of SEQ ID NO:76, the fragment comprising eight contiguous amino acids of SEQ ID NO:76; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo25\_1 deposited with the ATCC under accession number PTA-366; the protein being substantially free from other mammalian proteins.

86. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:27;
- (b) the nucleotide sequence of SEQ ID NO:27 from nucleotide 26 to nucleotide 307;
- (c) the nucleotide sequence of SEQ ID NO:27 from nucleotide 101 to nucleotide 307;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vo26\_1 deposited with the ATCC under accession number PTA-366;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo26\_1 deposited with the ATCC under accession number PTA-366;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vo26\_1 deposited with the ATCC under accession number PTA-366;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vo26\_1 deposited with the ATCC under accession number PTA-366;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:78;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:78, the fragment comprising eight contiguous amino acids of SEQ ID NO:78;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:27.

87. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:78;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:78, the fragment comprising eight contiguous amino acids of SEQ ID NO:78; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone vo26\_1 deposited with the ATCC under accession number PTA-366;
- the protein being substantially free from other mammalian proteins.

88. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:79;
- (b) the nucleotide sequence of SEQ ID NO:79 from nucleotide 43 to nucleotide 228;
- (c) the nucleotide sequence of SEQ ID NO:79 from nucleotide 94 to nucleotide 228;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vp23\_1 deposited with the ATCC under accession number PTA-368;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vp23\_1 deposited with the ATCC under accession number PTA-368;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vp23\_1 deposited with the ATCC under accession number PTA-368;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vp23\_1 deposited with the ATCC under accession number PTA-368;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:80;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80, the fragment comprising eight contiguous amino acids of SEQ ID NO:80;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:79.

89. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:80;

(b) a fragment of the amino acid sequence of SEQ ID NO:80, the fragment comprising eight contiguous amino acids of SEQ ID NO:80; and

(c) the amino acid sequence encoded by the cDNA insert of clone vp23\_1 deposited with the ATCC under accession number PTA-368;

the protein being substantially free from other mammalian proteins.

90. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:81;

(b) the nucleotide sequence of SEQ ID NO:81 from nucleotide 245 to nucleotide 427;

(c) the nucleotide sequence of SEQ ID NO:81 from nucleotide 308 to nucleotide 427;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vq7\_1 deposited with the ATCC under accession number PTA-368;

- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vq7\_1 deposited with the ATCC under accession number PTA-368;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vq7\_1 deposited with the ATCC under accession number PTA-368;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vq7\_1 deposited with the ATCC under accession number PTA-368;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:82;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:82, the fragment comprising eight contiguous amino acids of SEQ ID NO:82;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:81.

91. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:82;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:82, the fragment comprising eight contiguous amino acids of SEQ ID NO:82; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone vq7\_1 deposited with the ATCC under accession number PTA-368;
- the protein being substantially free from other mammalian proteins.

92. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:83;
- (b) the nucleotide sequence of SEQ ID NO:83 from nucleotide 119 to nucleotide 475;
- (c) the nucleotide sequence of SEQ ID NO:83 from nucleotide 185 to nucleotide 475;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vq8\_1 deposited with the ATCC under accession number PTA-368;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vq8\_1 deposited with the ATCC under accession number PTA-368;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vq8\_1 deposited with the ATCC under accession number PTA-368;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vq8\_1 deposited with the ATCC under accession number PTA-368;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:84;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:84, the fragment comprising eight contiguous amino acids of SEQ ID NO:84;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:83.

93. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:84;



- (b) a fragment of the amino acid sequence of SEQ ID NO:84, the fragment comprising eight contiguous amino acids of SEQ ID NO:84; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone vq8\_1 deposited with the ATCC under accession number PTA-368;
- the protein being substantially free from other mammalian proteins.

94. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:85;
- (b) the nucleotide sequence of SEQ ID NO:85 from nucleotide 90 to nucleotide 323;
- (c) the nucleotide sequence of SEQ ID NO:85 from nucleotide 141 to nucleotide 323;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vq9\_1 deposited with the ATCC under accession number PTA-368;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vq9\_1 deposited with the ATCC under accession number PTA-368;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vq9\_1 deposited with the ATCC under accession number PTA-368;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vq9\_1 deposited with the ATCC under accession number PTA-368;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:86;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:86, the fragment comprising eight contiguous amino acids of SEQ ID NO:86;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:85.

95. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:86;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:86, the fragment comprising eight contiguous amino acids of SEQ ID NO:86; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone vq9\_1 deposited with the ATCC under accession number PTA-368;
- the protein being substantially free from other mammalian proteins.

96. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:87;
- (b) the nucleotide sequence of SEQ ID NO:87 from nucleotide 18 to nucleotide 452;
- (c) the nucleotide sequence of SEQ ID NO:87 from nucleotide 72 to nucleotide 452;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vq10\_1 deposited with the ATCC under accession number PTA-368;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vq10\_1 deposited with the ATCC under accession number PTA-368;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vq10\_1 deposited with the ATCC under accession number PTA-368;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vq10\_1 deposited with the ATCC under accession number PTA-368;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:88;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88, the fragment comprising eight contiguous amino acids of SEQ ID NO:88;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:87.

97. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:88;

(b) a fragment of the amino acid sequence of SEQ ID NO:88, the fragment comprising eight contiguous amino acids of SEQ ID NO:88; and

(c) the amino acid sequence encoded by the cDNA insert of clone vq10\_1 deposited with the ATCC under accession number PTA-368;

the protein being substantially free from other mammalian proteins.

98. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:89;

(b) the nucleotide sequence of SEQ ID NO:89 from nucleotide 196 to nucleotide 378;

(c) the nucleotide sequence of SEQ ID NO:89 from nucleotide 262 to nucleotide 378;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vq13\_1 deposited with the ATCC under accession number PTA-368;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vq13\_1 deposited with the ATCC under accession number PTA-368;

(f) the nucleotide sequence of a mature protein coding sequence of clone vq13\_1 deposited with the ATCC under accession number PTA-368;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vq13\_1 deposited with the ATCC under accession number PTA-368;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:90;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:90, the fragment comprising eight contiguous amino acids of SEQ ID NO:90;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:89.

99. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:90;

(b) a fragment of the amino acid sequence of SEQ ID NO:90, the fragment comprising eight contiguous amino acids of SEQ ID NO:90; and

(c) the amino acid sequence encoded by the cDNA insert of clone vq13\_1 deposited with the ATCC under accession number PTA-368;

the protein being substantially free from other mammalian proteins.

100. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:91;
- (b) the nucleotide sequence of SEQ ID NO:91 from nucleotide 35 to nucleotide 718;
- (c) the nucleotide sequence of SEQ ID NO:91 from nucleotide 173 to nucleotide 718;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vq16\_1 deposited with the ATCC under accession number PTA-368;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vq16\_1 deposited with the ATCC under accession number PTA-368;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vq16\_1 deposited with the ATCC under accession number PTA-368;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vq16\_1 deposited with the ATCC under accession number PTA-368;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:92;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:92, the fragment comprising eight contiguous amino acids of SEQ ID NO:92;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:91.

101. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:92;

- (b) a fragment of the amino acid sequence of SEQ ID NO:92, the fragment comprising eight contiguous amino acids of SEQ ID NO:92; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone vq16\_1 deposited with the ATCC under accession number PTA-368;
- the protein being substantially free from other mammalian proteins.

102. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:93;
- (b) the nucleotide sequence of SEQ ID NO:93 from nucleotide 1 to nucleotide 762;
- (c) the nucleotide sequence of SEQ ID NO:93 from nucleotide 70 to nucleotide 762;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vq19\_1 deposited with the ATCC under accession number PTA-368;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vq19\_1 deposited with the ATCC under accession number PTA-368;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vq19\_1 deposited with the ATCC under accession number PTA-368;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vq19\_1 deposited with the ATCC under accession number PTA-368;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:94;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:94, the fragment comprising eight contiguous amino acids of SEQ ID NO:94;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:93.

103. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:94;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:94, the fragment comprising eight contiguous amino acids of SEQ ID NO:94; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone vq19\_1 deposited with the ATCC under accession number PTA-368;
- the protein being substantially free from other mammalian proteins.

104. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:95;
- (b) the nucleotide sequence of SEQ ID NO:95 from nucleotide 106 to nucleotide 792;
- (c) the nucleotide sequence of SEQ ID NO:95 from nucleotide 172 to nucleotide 792;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vq20\_1 deposited with the ATCC under accession number PTA-368;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vq20\_1 deposited with the ATCC under accession number PTA-368;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vq20\_1 deposited with the ATCC under accession number PTA-368;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vq20\_1 deposited with the ATCC under accession number PTA-368;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:96;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96, the fragment comprising eight contiguous amino acids of SEQ ID NO:96;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:95.

105. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:96;

(b) a fragment of the amino acid sequence of SEQ ID NO:96, the fragment comprising eight contiguous amino acids of SEQ ID NO:96; and

(c) the amino acid sequence encoded by the cDNA insert of clone vq20\_1 deposited with the ATCC under accession number PTA-368;

the protein being substantially free from other mammalian proteins.

106. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:97;

(b) the nucleotide sequence of SEQ ID NO:97 from nucleotide 40 to nucleotide 315;

(c) the nucleotide sequence of SEQ ID NO:97 from nucleotide 124 to nucleotide 315;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vq21\_1 deposited with the ATCC under accession number PTA-368;



(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vq21\_1 deposited with the ATCC under accession number PTA-368;

(f) the nucleotide sequence of a mature protein coding sequence of clone vq21\_1 deposited with the ATCC under accession number PTA-368;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vq21\_1 deposited with the ATCC under accession number PTA-368;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:98;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:98, the fragment comprising eight contiguous amino acids of SEQ ID NO:98;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:97.

107. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:98;

(b) a fragment of the amino acid sequence of SEQ ID NO:98, the fragment comprising eight contiguous amino acids of SEQ ID NO:98; and

(c) the amino acid sequence encoded by the cDNA insert of clone vq21\_1 deposited with the ATCC under accession number PTA-368;

the protein being substantially free from other mammalian proteins.

108. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:99;
- (b) the nucleotide sequence of SEQ ID NO:99 from nucleotide 70 to nucleotide 699;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone vr2\_1 deposited with the ATCC under accession number PTA-368;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vr2\_1 deposited with the ATCC under accession number PTA-368;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:100;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:100, the fragment comprising eight contiguous amino acids of SEQ ID NO:100;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:99.

109. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:100;
- (b) a fragment of the amino acid sequence of SEQ ID NO:100, the fragment comprising eight contiguous amino acids of SEQ ID NO:100; and
- (c) the amino acid sequence encoded by the cDNA insert of clone vr2\_1 deposited with the ATCC under accession number PTA-368;

the protein being substantially free from other mammalian proteins.

110. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:101;
- (b) the nucleotide sequence of SEQ ID NO:101 from nucleotide 170 to nucleotide 394;
- (c) the nucleotide sequence of SEQ ID NO:101 from nucleotide 227 to nucleotide 394;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone PTA-1075 deposited with the ATCC under accession number PTA-1075;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vc69\_1 deposited with the ATCC under accession number PTA-1075;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vc69\_1 deposited with the ATCC under accession number PTA-1075;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vc69\_1 deposited with the ATCC under accession number PTA-1075;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:102;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:102, the fragment comprising eight contiguous amino acids of SEQ ID NO:102;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:101.

111. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:102;

- (b) a fragment of the amino acid sequence of SEQ ID NO:102, the fragment comprising eight contiguous amino acids of SEQ ID NO:102; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone vc69\_1 deposited with the ATCC under accession number PTA-1075;
- the protein being substantially free from other mammalian proteins.

112. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:103;
- (b) the nucleotide sequence of SEQ ID NO:103 from nucleotide 43 to nucleotide 198;
- (c) the nucleotide sequence of SEQ ID NO:103 from nucleotide 85 to nucleotide 198;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vc71\_1 deposited with the ATCC under accession number PTA-1075;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vc71\_1 deposited with the ATCC under accession number PTA-1075;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vc71\_1 deposited with the ATCC under accession number PTA-1075;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vc71\_1 deposited with the ATCC under accession number PTA-1075;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:104;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:104, the fragment comprising eight contiguous amino acids of SEQ ID NO:104;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:103.

113. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:104;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:104, the fragment comprising eight contiguous amino acids of SEQ ID NO:104; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone vc71\_1 deposited with the ATCC under accession number PTA-1075;
- the protein being substantially free from other mammalian proteins.

114. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:105;
- (b) the nucleotide sequence of SEQ ID NO:105 from nucleotide 260 to nucleotide 1552;
- (c) the nucleotide sequence of SEQ ID NO:105 from nucleotide 335 to nucleotide 1552;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vo27\_1 deposited with the ATCC under accession number PTA-1075;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo27\_1 deposited with the ATCC under accession number PTA-1075;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vo27\_1 deposited with the ATCC under accession number PTA-1075;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vo27\_1 deposited with the ATCC under accession number PTA-1075;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:106;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:106, the fragment comprising eight contiguous amino acids of SEQ ID NO:106;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:105.

115. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:106;

(b) a fragment of the amino acid sequence of SEQ ID NO:106, the fragment comprising eight contiguous amino acids of SEQ ID NO:106; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo27\_1 deposited with the ATCC under accession number PTA-1075;

the protein being substantially free from other mammalian proteins.

116. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:107;

(b) the nucleotide sequence of SEQ ID NO:107 from nucleotide 15 to nucleotide 320;

(c) the nucleotide sequence of SEQ ID NO:107 from nucleotide 72 to nucleotide 320;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vo31\_1 deposited with the ATCC under accession number PTA-1075;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo31\_1 deposited with the ATCC under accession number PTA-1075;

(f) the nucleotide sequence of a mature protein coding sequence of clone vo31\_1 deposited with the ATCC under accession number PTA-1075;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vo31\_1 deposited with the ATCC under accession number PTA-1075;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:108;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:108, the fragment comprising eight contiguous amino acids of SEQ ID NO:108;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:107.

117. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:108;

(b) a fragment of the amino acid sequence of SEQ ID NO:108, the fragment comprising eight contiguous amino acids of SEQ ID NO:108; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo31\_1 deposited with the ATCC under accession number PTA-1075;

the protein being substantially free from other mammalian proteins.

118. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:109;
- (b) the nucleotide sequence of SEQ ID NO:109 from nucleotide 38 to nucleotide 1255;
- (c) the nucleotide sequence of SEQ ID NO:109 from nucleotide 86 to nucleotide 1255;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vo32\_1 deposited with the ATCC under accession number PTA-1075;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo32\_1 deposited with the ATCC under accession number PTA-1075;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vo32\_1 deposited with the ATCC under accession number PTA-1075;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vo32\_1 deposited with the ATCC under accession number PTA-1075;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:110;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:110, the fragment comprising eight contiguous amino acids of SEQ ID NO:110;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:109.

119. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:110;



- (b) a fragment of the amino acid sequence of SEQ ID NO:110, the fragment comprising eight contiguous amino acids of SEQ ID NO:110; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone vo32\_1 deposited with the ATCC under accession number PTA-1075;
- the protein being substantially free from other mammalian proteins.

120. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:111;
- (b) the nucleotide sequence of SEQ ID NO:111 from nucleotide 80 to nucleotide 1276;
- (c) the nucleotide sequence of SEQ ID NO:111 from nucleotide 131 to nucleotide 1276;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vo33\_1 deposited with the ATCC under accession number PTA-1075;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo33\_1 deposited with the ATCC under accession number PTA-1075;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vo33\_1 deposited with the ATCC under accession number PTA-1075;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vo33\_1 deposited with the ATCC under accession number PTA-1075;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:112;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:112, the fragment comprising eight contiguous amino acids of SEQ ID NO:112;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:111.

121. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:112;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:112, the fragment comprising eight contiguous amino acids of SEQ ID NO:112; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone vo33\_1 deposited with the ATCC under accession number PTA-1075;
- the protein being substantially free from other mammalian proteins.

122. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:113;
- (b) the nucleotide sequence of SEQ ID NO:113 from nucleotide 202 to nucleotide 429;
- (c) the nucleotide sequence of SEQ ID NO:113 from nucleotide 292 to nucleotide 429;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vq23\_1 deposited with the ATCC under accession number PTA-1075;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vq23\_1 deposited with the ATCC under accession number PTA-1075;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vq23\_1 deposited with the ATCC under accession number PTA-1075;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vq23\_1 deposited with the ATCC under accession number PTA-1075;

- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:114;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:114, the fragment comprising eight contiguous amino acids of SEQ ID NO:114;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:113.

123. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:114;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:114, the fragment comprising eight contiguous amino acids of SEQ ID NO:114; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone vq23\_1 deposited with the ATCC under accession number PTA-1075;
- the protein being substantially free from other mammalian proteins.

124. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:115;
- (b) the nucleotide sequence of SEQ ID NO:115 from nucleotide 37 to nucleotide 1113;
- (c) the nucleotide sequence of SEQ ID NO:115 from nucleotide 88 to nucleotide 1113;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vq24\_1 deposited with the ATCC under accession number PTA-1075;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vq24\_1 deposited with the ATCC under accession number PTA-1075;

(f) the nucleotide sequence of a mature protein coding sequence of clone vq24\_1 deposited with the ATCC under accession number PTA-1075;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vq24\_1 deposited with the ATCC under accession number PTA-1075;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:116;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:116, the fragment comprising eight contiguous amino acids of SEQ ID NO:116;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:115.

125. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:116;

(b) a fragment of the amino acid sequence of SEQ ID NO:116, the fragment comprising eight contiguous amino acids of SEQ ID NO:116; and

(c) the amino acid sequence encoded by the cDNA insert of clone vq24\_1 deposited with the ATCC under accession number PTA-1075;

the protein being substantially free from other mammalian proteins.

126. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:117;
- (b) the nucleotide sequence of SEQ ID NO:117 from nucleotide 40 to nucleotide 207;
- (c) the nucleotide sequence of SEQ ID NO:117 from nucleotide 103 to nucleotide 207;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vq26\_1 deposited with the ATCC under accession number PTA-1075;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vq26\_1 deposited with the ATCC under accession number PTA-1075;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vq26\_1 deposited with the ATCC under accession number PTA-1075;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vq26\_1 deposited with the ATCC under accession number PTA-1075;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:118;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:118, the fragment comprising eight contiguous amino acids of SEQ ID NO:118;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:117.

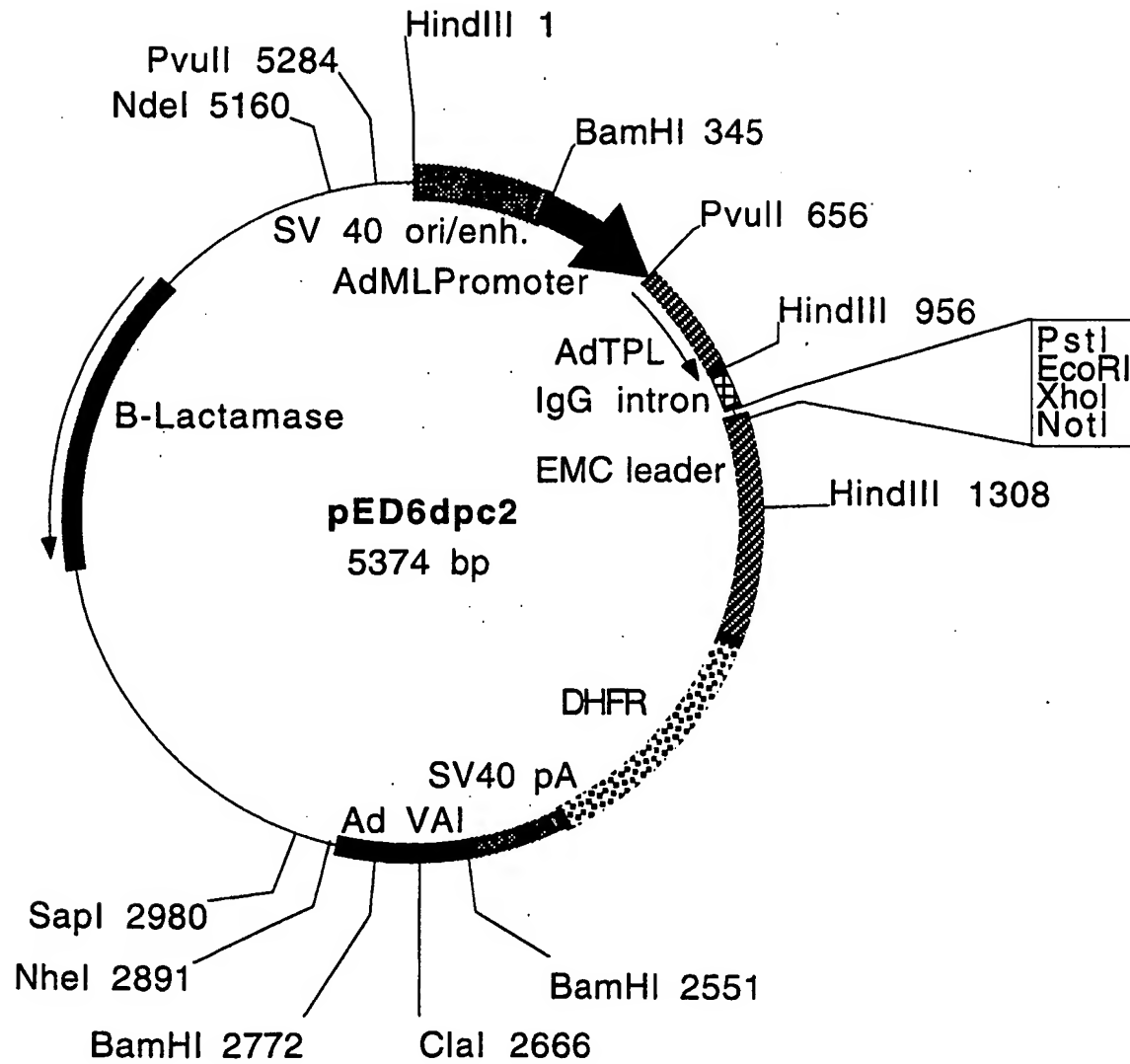
127. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:118;

(b) a fragment of the amino acid sequence of SEQ ID NO:118, the fragment comprising eight contiguous amino acids of SEQ ID NO:118; and

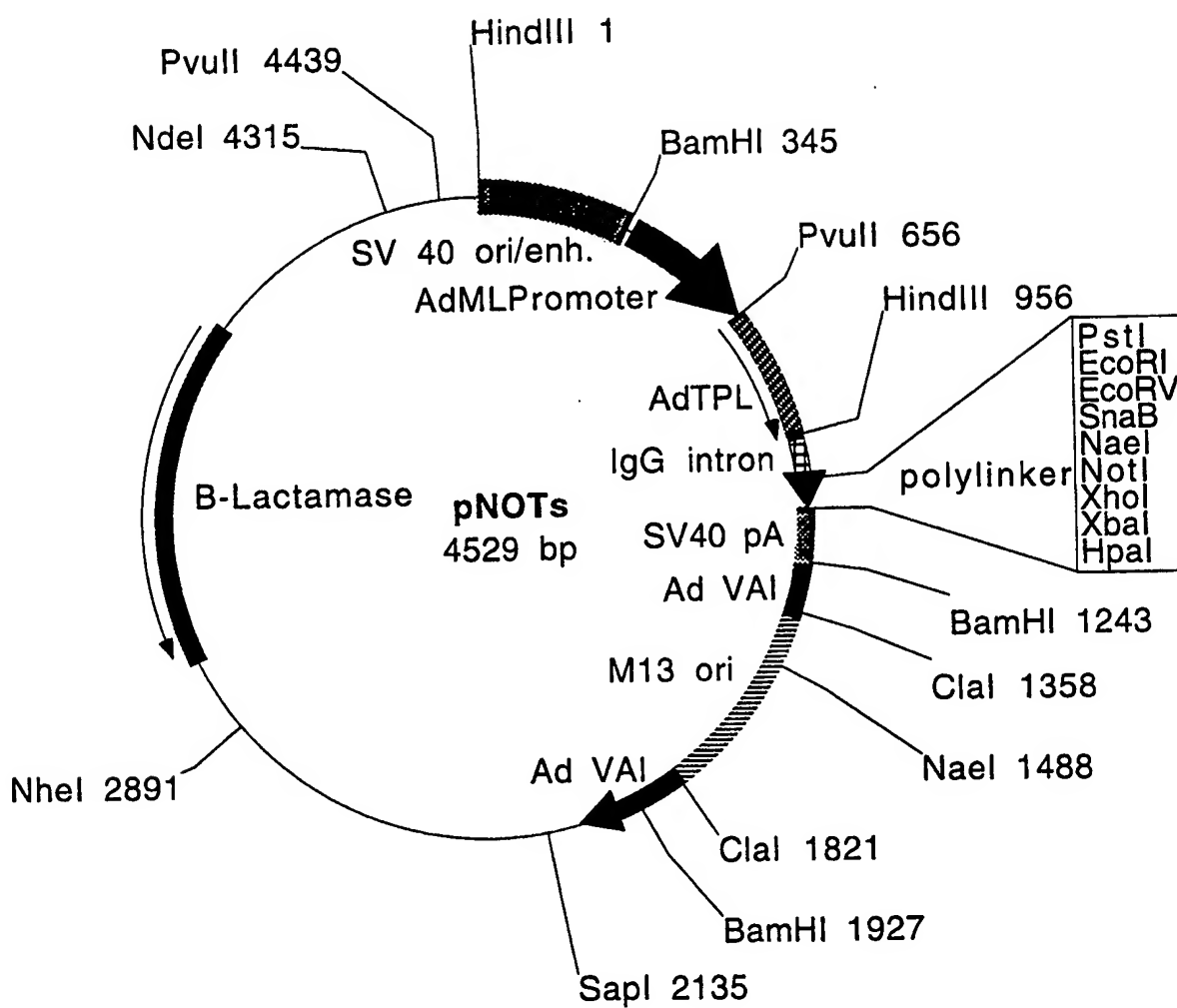
(c) the amino acid sequence encoded by the cDNA insert of clone vq26\_1 deposited with the ATCC under accession number PTA-1075; the protein being substantially free from other mammalian proteins.

Fig. 1A



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Fig. 1B



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## SEQUENCE LISTING

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 Hall, Jeff  
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tcctcacttt ctgatagtca gtttccccca gtctccagtt ttaccctgac ttagagtcca 2040
caaacttcat cagaccacct gtgctcatgg acgtgggtct ttctagaggg aagcctcggg 2100

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```

&lt;210&gt; 2

&lt;211&gt; 78

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2

```

Met Val Leu Thr Leu Trp Cys Asn Leu Cys Ser Arg Ala Ser Ser Trp
  1                      5                      10                     15

```

```

Val Arg Gln Lys His Val Ser Cys Cys Val His Asn Tyr Thr Gln Pro
          20                      25                     30

```

```

Phe Leu Leu Ile Gln Ser Ser Phe Trp Ala Met Ser Ser Glu Thr Lys
    35                      40                     45

```

```

Pro Lys Ala Leu Ser Lys Asp Tyr Leu Cys Ile Ser Tyr Arg Ser Pro
    50                      55                     60

```

```

His Ser Thr Pro Thr His Arg His Ser Ser Asn Arg Phe Leu
    65                      70                     75

```

&lt;210&gt; 3

&lt;211&gt; 1326

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3

```

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aaaaaa                                     1326

```

&lt;210&gt; 4

&lt;211&gt; 440

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 4

```

Met Ala Val Ser Glu Arg Arg Gly Leu Gly Arg Gly Ser Pro Ala Glu
  1              5              10             15

Trp Gly Gln Arg Leu Leu Leu Val Leu Leu Leu Gly Gly Cys Ser Gly
      20              25              30

Arg Ile His Arg Leu Ala Leu Thr Gly Glu Lys Arg Ala Asp Ile Gln
      35              40              45

Leu Asn Ser Phe Gly Phe Tyr Thr Asn Gly Ser Leu Glu Val Glu Leu
      50              55              60

Ser Val Leu Arg Leu Gly Leu Arg Glu Ala Glu Glu Lys Ser Leu Leu
      65              70              75              80

Val Gly Phe Ser Leu Ser Arg Val Arg Ser Gly Arg Val Arg Ser Tyr
      85              90              95

Ser Thr Arg Asp Phe Gln Asp Cys Pro Leu Gln Lys Asn Ser Ser Ser
      100             105             110

Phe Leu Val Leu Phe Leu Ile Asn Thr Lys Asp Leu Gln Val Gln Val
      115             120             125

Arg Lys Tyr Gly Glu Gln Lys Thr Leu Phe Ile Phe Pro Gly Leu Leu
      130             135             140

```

Pro Glu Ala Pro Ser Lys Pro Gly Leu Pro Lys Pro Gln Ala Thr Val  
 145 150 155 160  
 Pro Arg Lys Val Asp Gly Gly Gly Thr Ser Ala Ala Ser Lys Pro Lys  
 165 170 175  
 Ser Thr Pro Ala Val Ile Gln Gly Pro Ser Gly Lys Asp Lys Asp Leu  
 180 185 190  
 Val Leu Gly Leu Ser His Leu Asn Asn Ser Tyr Asn Phe Ser Phe His  
 195 200 205  
 Val Val Ile Gly Ser Gln Ala Glu Glu Gly Gln Tyr Ser Leu Asn Phe  
 210 215 220  
 His Asn Cys Asn Asn Ser Val Pro Gly Lys Glu His Pro Phe Asp Ile  
 225 230 235 240  
 Thr Val Met Ile Arg Glu Lys Asn Pro Asp Gly Phe Leu Ser Ala Ala  
 245 250 255  
 Glu Met Pro Leu Phe Lys Leu Tyr Met Val Met Ser Ala Cys Phe Leu  
 260 265 270  
 Ala Ala Gly Ser Gly Cys Thr Ser Ser Trp Trp Arg Ala Pro Pro Cys  
 275 280 285  
 Leu Leu Arg Ala His Gly Leu Gln Val Pro Ala His Arg Lys Gln Pro  
 290 295 300  
 Val Pro Ala Ala Ala Pro Gly Gly Arg Gly Gly Cys Ser Asp Gly Ala  
 305 310 315 320  
 Ser Asn Asp Gly Leu Trp Val Pro Gly Arg Pro Leu Gln Ser Gln Gln  
 325 330 335  
 Asn Ser Gln Arg Ala Gly Thr Val Met Ile Thr Ser Thr Ser Gln Thr  
 340 345 350  
 Lys Gly Ser Ser Ser Pro Ser Ile Ser His Ser Cys Pro Ser Ser Thr  
 355 360 365  
 Ala Tyr Val Gly Arg Trp Arg Gly Ser Met Trp Thr Arg Arg Pro Ala  
 370 375 380  
 Pro Arg Asp Pro Gly Ser Arg Thr Ser Pro Phe Gly Arg Arg Val Pro  
 385 390 395 400  
 Ser Ser Pro Gln Ile Leu Gly Ser Pro Val Leu Thr Pro Gly Pro Pro  
 405 410 415  
 Leu Pro Ser Ser Tyr Val Tyr Asn Asn Asp Gln Ser Val Trp Leu Lys  
 420 425 430  
 Lys Lys Lys Lys Lys Lys Lys Lys  
 435 440

&lt;210&gt; 5

<211> 1280  
 <212> DNA  
 <213> Homo sapiens

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 caacagaggg tacgttttct tgaagatgta tcttgtaaaa gaaaaaaatc ctttatttat 300  
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<210> 6  
 <211> 58  
 <212> PRT  
 <213> Homo sapiens

<400> 6  
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 Ala Ala Ser Thr His Cys Ile Cys Asp Lys Ala Asp Thr Arg Asp Asn  
 20 25 30  
 Arg Gly Tyr Val Phe Leu Lys Met Tyr Leu Val Lys Glu Lys Asn Pro  
 35 40 45  
 Leu Phe Ile Tyr Asp Gly Lys Leu Gly Thr  
 50 55

<210> 7  
 <211> 1001  
 <212> DNA  
 <213> Homo sapiens

<400> 7  
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 tcatccctgt gcaaatggaa gtacctgtac cactgtggcc aaccagttct cctgcaaatg 360  
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```

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1001

```

&lt;210&gt; 8

&lt;211&gt; 114

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 8

```

Met Pro Ala Cys Leu Ile Pro Val Gln Met Glu Val Pro Val Pro Leu
  1             5             10             15

```

```

Trp Pro Thr Ser Ser Pro Ala Asn Ala Ser Gln Ala Ser Gln Gly Arg
      20             25             30

```

```

Ser Val Arg Leu Met Ser Met Ser Val Thr Phe Gln Asp Thr Ala Ser
    35             40             45

```

```

Met Val Ala Pro Ala Ser Thr Cys Leu Val Pro Thr Ser Ala Ser Ala
    50             55             60

```

```

Phe Arg Ala Ser Gln Ala Ser Thr Val Thr Ala Cys Met Cys Pro Val
    65             70             75             80

```

```

His Pro Arg Leu Val Ser Met Glu Ala Pro Val Gly Arg Leu Val Thr
      85             90             95

```

```

Ser Leu Leu Ser Ala Thr Ala Phe Gln Val Arg Ser Ser Leu Val Ser
    100             105             110

```

Gln Asp

&lt;210&gt; 9

&lt;211&gt; 2058

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 9

```

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```

```

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```

&lt;210&gt; 10

&lt;211&gt; 96

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 10

```

Met Thr Phe Asp Phe Cys Cys Leu Tyr Phe Ser Thr Val Tyr Ala Pro
 1             5             10             15

```

```

Ser Phe Lys Tyr Ile Cys Val His Thr Asp Thr His Ile Cys Val Cys
      20             25             30

```

```

Val Cys Ile Tyr Leu Ser Ser Val Val Ser Lys Ser Ser Ala Glu Ala
      35             40             45

```

```

Asp Gly Val Leu Gln Pro Arg Arg His Pro Ala Ser Leu Leu Ile Val
      50             55             60

```

```

Phe Ala Thr Ser Ile Ser Glu Ser Ser Leu Leu Ile Phe Ser Phe Gln
      65             70             75             80

```

```

Lys Thr Glu Ala Lys Leu Ile Val Phe Ala Val Ser Leu Ala Ala Lys
      85             90             95

```

&lt;210&gt; 11

&lt;211&gt; 1498

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 11

```

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```

<210> 12

<211> 117

<212> PRT

<213> Homo sapiens

<400> 12

```

Met Ala Ala Ala Ala Glu Pro Met Gly Pro Ala Gln Val Pro Met Asn
  1              5              10              15

```

```

Ser Glu Val Ile Val Asp Pro Ile Gln Gly Gln Val Asn Phe Glu Asp
      20              25              30

```

```

Val Phe Val Tyr Phe Ser Gln Glu Glu Trp Val Leu Leu Asp Glu Ala
      35              40              45

```

```

Gln Arg Leu Leu Tyr Arg Asp Val Met Leu Glu Asn Phe Ala Leu Met
      50              55              60

```

```

Ala Ser Leu Gly Ile Pro Gln Thr Met Ala Ala Phe Gly Leu Lys Tyr
      65              70              75              80

```

```

Leu Leu Asn Asp Thr Gly Tyr Thr Ser Ser Lys Ser Asn Thr Ile Thr
      85              90              95

```

```

Ala Thr Asp Ser Pro Ala Asp Leu Pro Arg Lys Thr Glu Pro His Thr
      100             105             110

```

```

Pro Ser Trp Ser Trp
      115

```

<210> 13

<211> 1718

<212> DNA

<213> Homo sapiens

<400> 13

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```



```

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 <212> PRT  
 <213> Homo sapiens

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Ser Ile Cys Ser Ala Gly Ala Pro Ala Lys Tyr Ser Ile Thr Phe Thr
      35              40              45

Gly Lys Trp Ser Gln Thr Ala Ser Pro Ser Ser Thr Pro Cys Ser Ala
      50              55              60

Pro Leu Arg Ser Gly Leu Arg Cys Trp Gly Pro Arg Ile Ala Pro Thr
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Thr Ala Cys Gly Gly Arg Thr Ser Thr Ser Val Thr Gly Cys Ala Thr
      85              90              95

Leu Arg Ser Ala Ala Arg Pro Gly Arg
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 <212> DNA  
 <213> Homo sapiens

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847

&lt;210&gt; 16

&lt;211&gt; 189

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 16

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Met Arg Leu Ser Leu Pro Leu Leu Leu Leu Leu Gly Ala Trp Ala
  1              5              10              15

Ile Pro Gly Gly Leu Gly Asp Arg Ala Pro Leu Thr Ala Thr Ala Pro
      20              25              30

Gln Leu Asp Asp Glu Glu Met Tyr Ser Ala His Met Pro Ala His Leu
      35              40              45

Arg Cys Asp Ala Cys Arg Ala Val Ala Tyr Gln Met Trp Gln Asn Leu
      50              55              60

Ala Lys Ala Glu Thr Lys Leu His Thr Ser Asn Ser Gly Gly Arg Arg
      65              70              75              80

Glu Leu Ser Glu Leu Val Tyr Thr Asp Val Leu Asp Arg Ser Cys Ser
      85              90              95

Arg Asn Trp Gln Asp Tyr Gly Val Arg Glu Val Asp Gln Val Lys Arg
      100             105             110

Leu Thr Gly Pro Gly Leu Ser Glu Gly Pro Glu Pro Ser Ile Ser Val
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Met Val Thr Gly Gly Pro Trp Pro Thr Arg Leu Ser Arg Thr Cys Leu
      130             135             140

His Tyr Leu Gly Glu Phe Gly Glu Asp Gln Ile Tyr Glu Ala His Gln
      145             150             155             160

Gln Gly Arg Gly Ala Leu Glu Ala Leu Leu Cys Gly Gly Pro Gln Gly
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 <213> Homo sapiens

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 <211> 106  
 <212> PRT  
 <213> Homo sapiens

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 Ser Leu His Phe Pro Ser Ser Ser Asp Ser Pro Ala Ser Ala Ser Arg  
 35 40 45  
 Val Ala Gly Thr Thr Gly Ala Cys His His Ala Arg Leu Ile Phe Val  
 50 55 60  
 Phe Leu Val Glu Thr Glu Phe His Cys Val Gly Gln Asp Gly Leu Asp  
 65 70 75 80  
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 Arg Arg Glu Pro Pro Arg Leu Ala Tyr Val  
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<210> 19  
 <211> 2166  
 <212> DNA  
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 <212> PRT  
 <213> Homo sapiens

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 Trp Val Leu Thr Leu Thr Ala Glu Ser Gly Leu Ala Arg Thr Gln Ser  
 35 40 45

Lys Ser Val Phe Gln Leu Ser Ile Ser Leu Val Glu  
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 <212> DNA  
 <213> Homo sapiens

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 <212> PRT  
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 Ser Val Gly Ile Gly Val Pro Ile Met Leu Ala Tyr Val Tyr Gly Val  
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 Val Pro Ile Ser Leu Cys Arg Gly Gly Gly Cys Gly Val Ser Thr Ala  
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 85 90 95  
 Thr Val Ala Asp Ala Trp Arg Ala Leu Lys Asn Pro Ser Ile Gly Glu  
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Ser Ser Ile Glu Gly Leu Thr Ser Val Leu Ser Thr Ser Gly Ser Pro  
 115 120 125  
 Thr Asp Gly Leu Ser Val Met Gln Gly Pro Tyr Ser Glu Thr Ala Ser  
 130 135 140  
 Phe Ala Ala Leu Ser Gly Gly Thr Leu Ser Gly Gly Ile Leu Ser Ser  
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 Gly Lys Gly Lys Tyr Ser Arg Leu Glu Val Gln Ala Asp Val Gln Lys  
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 Ala Ser Thr Arg Ala Met Ala Gly Ser Ile Ile Ser Ser Tyr Asn Pro  
 195 200 205  
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 210 215 220  
 Lys Pro Ser His Tyr Gln Leu Val Ser Gly Ser Ser Thr Glu Asp Ser  
 225 230 235 240  
 Leu His Val His Ala Gln Met Ala Glu Asn Glu Glu Glu Gly Ser Gly  
 245 250 255  
 Gly Gly Gly Ser Glu Glu Asp Pro Pro Cys Arg His Gln Ser Cys Glu  
 260 265 270  
 Gln Lys Asp Cys Leu Ala Ser Lys Pro Trp Asp Ile Ser Leu Ala Gln  
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 Pro Glu Ser Ile Arg Ser Asp Leu Glu Ser Ser Asp Ala Gln Ser Asp  
 290 295 300  
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 305 310 315 320  
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<210> 25  
 <211> 2350  
 <212> DNA  
 <213> Homo sapiens

<400> 25  
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&lt;210&gt; 26

&lt;211&gt; 167

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 26

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Met Tyr His Gln Leu Leu Lys Phe Leu Ile Ile Gly His Leu Lys Leu
  1              5              10              15

```

```

Leu Arg Asp Phe Asp Phe Leu Gly Glu Asp Gly Val Cys His Leu Leu
      20              25              30

```

```

Ala Thr Ile Ile Ala Leu Ser Gln Ile Gln Lys Ile Leu Thr Lys Asn
  35              40              45

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```

Leu Lys Val Glu Ile Gln Asp His Gly Tyr Leu Pro His Leu Glu Ile
  50              55              60

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```

Asp Ala His Leu Cys Ser Leu Glu Gly Gly Glu Arg Glu Glu Met Asn
  65              70              75              80

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Leu Gln Gly Tyr Leu Pro Leu Ile His His Leu Asp Leu Ile Phe Leu
  85              90              95

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Glu Glu Asn Gln Met Lys Trp Phe Thr Leu Lys His Arg Met Ile Leu  
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Leu Glu Leu Leu Pro Thr Asp His Lys His Leu Gln His Gln Ala Val  
 115 120 125

Pro Gln Gln Val Ala Leu His Gln Ile Arg Leu Lys Val Glu Glu Ile  
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Gln Glu Tyr Gln Gly Phe Phe Leu Val Pro Tyr Ser Gly Leu Gln Ser  
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Pro Gln His Leu Gly Val Ile  
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<210> 27

<211> 1635

<212> DNA

<213> Homo sapiens

<400> 27

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<210> 28

<211> 89

<212> PRT

<213> Homo sapiens

<400> 28

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Leu Ser Leu Ser Ser Ile Pro Met Leu Ile Gly Arg Gln Asp Ala Leu  
 35 40 45

Ile Lys Pro Gln Gly Ile Arg Gly Leu Val Leu Gln His Pro Val Leu  
 50 55 60

Thr Cys Cys Val Thr Leu Glu Tyr Phe Leu Ala Ser Leu Gly Phe Arg  
 65 70 75 80

Arg Cys Leu Tyr Thr Leu Val Cys Tyr  
 85

&lt;210&gt; 29

&lt;211&gt; 3415

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 29

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&lt;210&gt; 30

&lt;211&gt; 55

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 30

```

Met Phe Met Lys Ile Tyr Thr Ser Ser Val Pro Leu Phe Arg Gly Met
  1             5             10             15

```

```

Leu Ser Cys Leu Ala Leu Ser Cys Trp Cys Ser Leu Ser Ala Pro Leu
      20             25             30

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Ser Ser Trp Val Asn Gly Asp Cys Gly Ser Cys Leu Ser Ile Ser Asp
      35             40             45

```

```

Ser Ser Asn Asp Thr Gly Lys
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&lt;210&gt; 31

&lt;211&gt; 2967

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 31

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&lt;210&gt; 32

&lt;211&gt; 250

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 32

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Met Ala Arg Cys Phe Ser Leu Val Leu Leu Leu Thr Ser Ile Trp Thr
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Thr Arg Leu Leu Val Gln Gly Ser Leu Arg Ala Glu Glu Leu Ser Ile
      20                      25                      30

Gln Val Ser Cys Arg Ile Met Gly Ile Thr Leu Val Ser Lys Lys Ala
      35                      40                      45

Asn Gln Gln Leu Asn Phe Thr Glu Ala Lys Glu Ala Cys Arg Leu Leu
      50                      55                      60

Gly Leu Ser Leu Ala Gly Lys Asp Gln Val Glu Thr Ala Leu Lys Ala
      65                      70                      75                      80

Ser Phe Glu Thr Cys Ser Tyr Gly Trp Val Gly Asp Gly Phe Val Val
      85                      90                      95

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Ile Ser Arg Ile Ser Pro Asn Pro Lys Cys Gly Lys Asn Gly Val Gly  
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 Tyr Asn Ser Ser Asp Thr Trp Thr Asn Ser Cys Ile Pro Glu Ile Ile  
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 Thr Thr Lys Asp Pro Ile Phe Asn Thr Gln Thr Ala Thr Gln Thr Thr  
 145 150 155 160  
 Glu Phe Ile Val Ser Asp Ser Thr Tyr Ser Val Ala Ser Pro Tyr Ser  
 165 170 175  
 Thr Ile Pro Ala Pro Thr Thr Thr Pro Pro Ala Pro Ala Ser Thr Ser  
 180 185 190  
 Ile Pro Arg Arg Lys Lys Leu Ile Cys Val Thr Glu Val Phe Met Glu  
 195 200 205  
 Thr Ser Thr Met Ser Thr Glu Thr Glu Pro Phe Val Glu Asn Lys Ala  
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 <213> Homo sapiens

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&lt;210&gt; 34

&lt;211&gt; 55

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 34

```

Met Lys Leu Gln Leu Trp Tyr Val Cys Val Ile Leu Phe Leu Ile Gly
  1              5              10              15

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Ile Ser Leu Leu Ala Val Gly Thr Asp Ser Asp Gly Asn Val Ala Thr
      20              25              30

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Glu Cys Phe Leu Ser Phe Leu Val Pro Ser Ile Phe Ile Ser Thr Phe
    35              40              45

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```

Leu Val Cys Cys Pro Leu Phe
    50              55

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&lt;210&gt; 35

&lt;211&gt; 3283

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 35

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<210> 36  
 <211> 79  
 <212> PRT  
 <213> Homo sapiens

<400> 36  
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 Leu Leu Leu Ala Val Val Gln Phe Thr Val Ser Lys Arg Lys Ile Asn  
 20 25 30

Tyr Phe Ser Glu Lys Val His Pro Phe Leu Val Leu Arg Thr Ile Lys  
 35 40 45

Ile His Tyr Asp Glu Leu Tyr Leu Ile Tyr Val Tyr Phe Asp Thr Gly  
 50 55 60

Phe Lys Glu His Leu Arg Glu Glu Cys Ser Leu Asp Leu Leu Asn  
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<210> 37

<211> 2248

<212> DNA

<213> Homo sapiens

<400> 37

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<210> 38

<211> 119

<212> PRT

<213> Homo sapiens



&lt;400&gt; 38

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Gly Ala Pro Gly Pro Ala Asn Ile Ser Gly Arg Met Gln Lys Val Ser  
 35 40 45

Tyr Phe His Cys Thr Leu Ile Gly Tyr Phe Val Gly Leu Leu Thr Ala  
 50 55 60

Thr Val Ala Ser Arg Ile His Arg Ala Ala Gln Pro Ala Leu Leu Tyr  
 65 70 75 80

Leu Val Pro Phe Thr Leu Leu Pro Leu Leu Thr Met Ala Tyr Leu Lys  
 85 90 95

Gly Asp Leu Arg Arg Met Trp Ser Glu Pro Phe His Ser Lys Ser Ser  
 100 105 110

Ser Ser Arg Phe Leu Glu Val  
 115

&lt;210&gt; 39

&lt;211&gt; 931

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 39

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 aaaaaaaaa aaaaaaaaa aaaaaaaaa a 931

&lt;210&gt; 40

&lt;211&gt; 53

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 40

Met Ala Ser Pro Ser Leu Ala Leu Ile Trp Ala Pro Ala Leu Ser Ile  
 1 5 10 15

Ala Val Thr Ser Leu Thr Thr Leu Ile Ser Gln Pro Cys Leu Phe Phe

20

25

30

Leu Thr Leu Ser Pro Pro Pro Leu Arg Arg His Cys Arg Gly Pro Pro  
 35 40 45

Gly Arg Arg Leu Ser  
 50

&lt;210&gt; 41

&lt;211&gt; 3625

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 41

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&lt;210&gt; 42

&lt;211&gt; 488

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 42

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Met Ala Gly Lys Gly Ser Ser Gly Arg Arg Pro Leu Leu Leu Gly Leu
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Val Glu Glu Ser Phe Asn Leu Gln Ala Thr His Asp Leu Leu Tyr His
  35                      40                      45

Trp Gln Asp Leu Glu Gln Tyr Asp His Leu Glu Phe Pro Gly Val Val
  50                      55                      60

Pro Arg Thr Phe Leu Gly Pro Val Val Ile Ala Val Phe Ser Ser Pro
  65                      70                      75                      80

Ala Val Tyr Val Leu Ser Leu Leu Glu Met Ser Lys Phe Tyr Ser Gln
                85                      90                      95

Leu Ile Val Arg Gly Val Leu Gly Leu Gly Val Ile Phe Gly Leu Trp
  100                      105                      110

Thr Leu Gln Lys Glu Val Arg Arg His Phe Gly Ala Met Val Ala Thr
  115                      120                      125

Met Phe Cys Trp Val Thr Ala Met Gln Phe His Leu Met Phe Tyr Cys
  130                      135                      140

Thr Arg Thr Leu Pro Asn Val Leu Ala Leu Pro Val Val Leu Leu Ala
  145                      150                      155                      160

Leu Ala Ala Trp Leu Arg His Glu Trp Ala Arg Phe Ile Trp Leu Ser
                165                      170                      175

Ala Phe Ala Ile Ile Val Phe Arg Val Glu Leu Cys Leu Phe Leu Gly
  180                      185                      190

Leu Leu Leu Leu Leu Ala Leu Gly Asn Arg Lys Val Ser Val Val Arg

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195	200	205
Ala Leu Arg His Ala Val Pro Ala Gly Ile Leu Cys Leu Gly Leu Thr 210	215	220
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Lys Val Leu Trp Tyr Asn Thr Val Leu Asn Lys Ser Ser Asn Trp Gly 245	250	255
Thr Ser Pro Leu Leu Trp Tyr Phe Tyr Ser Ala Leu Pro Arg Gly Leu 260	265	270
Gly Cys Ser Leu Leu Phe Ile Pro Leu Gly Leu Val Asp Arg Arg Thr 275	280	285
His Ala Pro Thr Val Leu Ala Leu Gly Phe Met Ala Leu Tyr Ser Leu 290	295	300
Leu Pro His Lys Glu Leu Arg Phe Ile Ile Tyr Ala Phe Pro Met Leu 305	310	315 320
Asn Ile Thr Ala Ala Arg Gly Cys Ser Tyr Leu Leu Asn Asn Tyr Lys 325	330	335
Lys Ser Trp Leu Tyr Lys Ala Gly Ser Leu Leu Val Ile Gly His Leu 340	345	350
Val Val Asn Ala Ala Tyr Ser Ala Thr Ala Leu Tyr Val Ser His Phe 355	360	365
Asn Tyr Pro Gly Gly Val Ala Met Gln Arg Leu His Gln Leu Val Pro 370	375	380
Pro Gln Thr Asp Val Leu Leu His Ile Asp Val Ala Ala Ala Gln Thr 385	390	395 400
Gly Val Ser Arg Phe Leu Gln Val Asn Ser Ala Trp Arg Tyr Asp Lys 405	410	415
Arg Glu Asp Val Gln Pro Gly Thr Gly Met Leu Ala Tyr Thr His Ile 420	425	430
Leu Met Glu Ala Ala Pro Gly Leu Leu Ala Leu Tyr Arg Asp Thr His 435	440	445
Arg Val Leu Ala Ser Val Val Gly Thr Thr Gly Val Ser Leu Asn Leu 450	455	460
Thr Gln Leu Pro Pro Phe Asn Val His Leu Gln Thr Lys Leu Val Leu 465	470	475 480
Leu Glu Arg Leu Pro Arg Pro Ser 485		

<210> 43  
 <211> 2861  
 <212> DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 43

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&lt;210&gt; 44

&lt;211&gt; 84

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 44

Met Lys Phe His Ile Lys Asn Asp Asp Lys Phe Thr His Cys Ala Ile  
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Ser Gln Ser Glu Asn Lys Val Glu Leu Ala Val Phe Ser Leu Leu Leu  
 20 25 30

Ser Glu His Trp Asp Asn Trp Ser Phe Lys Asn Ile His Pro Leu Thr  
 35 40 45

Ala Ser Leu Ser Gly Tyr Phe Tyr Leu Cys Val Gln Arg His Phe Phe  
 50 55 60

Ser Ala Val Ile Ile Ile Thr Ser Gln Lys Lys Met Leu Thr Asp Leu  
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Leu Thr Gly Pro

<210> 45

<211> 1556

<212> DNA

<213> Homo sapiens

<400> 45

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<210> 46

<211> 224

<212> PRT

<213> Homo sapiens

<400> 46

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Met Val Ala Gly Met Val Val Phe Tyr Gly Gly Ala Ser Leu Val Tyr		
35	40	45
Arg Leu Pro Gln Ser Trp Val Gly Pro Lys Leu Pro Trp Lys Leu Leu		
50	55	60
His Ala Ala Leu His Leu Met Ala Phe Val Leu Thr Val Val Gly Leu		
65	70	75
Val Ala Val Phe Thr Phe His Asn His Gly Arg Thr Ala Asn Leu Tyr		
85	90	95
Ser Leu His Ser Trp Leu Gly Ile Thr Thr Val Phe Leu Phe Ala Cys		
100	105	110
Gln Trp Phe Leu Gly Phe Ala Val Phe Leu Leu Pro Trp Ala Ser Met		
115	120	125
Trp Leu Arg Ser Leu Leu Lys Pro Ile His Val Phe Phe Gly Ala Ala		
130	135	140
Ile Leu Ser Leu Ser Ile Ala Ser Val Ile Ser Gly Ile Asn Glu Lys		
145	150	155
Leu Phe Phe Ser Leu Lys Asn Thr Thr Arg Pro Tyr His Ser Leu Pro		
165	170	175
Ser Glu Ala Val Phe Ala Asn Ser Thr Gly Met Leu Val Val Ala Phe		
180	185	190
Gly Leu Leu Val Leu Tyr Ile Leu Leu Ala Ser Ser Trp Lys Arg Pro		
195	200	205
Glu Pro Gly Ile Leu Thr Asp Arg Gln Pro Leu Leu His Asp Gly Glu		
210	215	220

&lt;210&gt; 47

&lt;211&gt; 2446

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 47

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<210> 48  
 <211> 74  
 <212> PRT  
 <213> Homo sapiens

<400> 48  
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 His Ser Pro Leu Leu Ser Gln Ala Leu Gly Cys Gly Phe Ile Phe Pro  
 35 40 45  
 Ser Ser Leu Thr Thr Gln Glu Ala Gln Ser Phe Ser Leu Lys Lys Gly  
 50 55 60  
 Gly Pro Ala Leu Phe Pro Leu Leu Gln Asn  
 65 70

<210> 49  
 <211> 1231  
 <212> DNA  
 <213> Homo sapiens

<400> 49  
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&lt;210&gt; 50

&lt;211&gt; 113

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 50

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  1                      5                      10                     15

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Leu Tyr Leu Phe Gln Leu His Met Lys Leu Tyr Met Val Pro Trp Pro
      20                      25                      30

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Leu Val Leu Met Ile Phe Asn Ile Ser Ala Thr Val Leu Tyr Ile Thr
      35                      40                      45

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Ala Phe Ile Ala Cys Ser Ala Ala Val Asp Leu Thr Ser Leu Arg Gly
      50                      55                      60

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Thr Arg Pro Tyr Asn Gln Arg Ala Ala Ala Ser Phe Phe Ala Cys Leu
      65                      70                      75                      80

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Val Met Ile Ala Tyr Gly Val Ser Ala Phe Phe Ser Tyr Gln Ala Trp
      85                      90                      95

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Arg Gly Val Gly Ser Asn Ala Ala Thr Ser Gln Met Ala Gly Gly Tyr
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Ala

&lt;210&gt; 51

&lt;211&gt; 3290

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 51

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&lt;210&gt; 52

&lt;211&gt; 518

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 52

Met Pro Val Ser Pro Leu Ala Val Ala Met Leu Ala Cys Ala Arg

1

5

10

15

Ile Gly Ala Val His Thr Val Ile Phe Ala Gly Phe Ser Ala Glu Ser

20	25	30
Leu Ala Gly Arg Ile Asn Asp Ala Lys Cys Lys Val Val Ile Thr Phe 35 40 45		
Asn Gln Gly Leu Arg Gly Gly Arg Val Val Glu Leu Lys Lys Ile Val 50 55 60		
Asp Glu Ala Val Lys His Cys Pro Thr Val Gln His Val Leu Val Ala 65 70 75 80		
His Arg Thr Asp Asn Lys Val His Met Gly Asp Leu Asp Val Pro Leu 85 90 95		
Glu Gln Glu Met Ala Lys Glu Asp Pro Val Cys Ala Pro Glu Ser Met 100 105 110		
Gly Ser Glu Asp Met Leu Phe Met Leu Tyr Thr Ser Gly Ser Thr Gly 115 120 125		
Met Pro Lys Gly Ile Val His Thr Gln Ala Gly Tyr Leu Leu Tyr Ala 130 135 140		
Ala Leu Thr His Lys Leu Val Phe Asp His Gln Pro Gly Asp Ile Phe 145 150 155 160		
Gly Cys Val Ala Asp Ile Gly Trp Ile Thr Gly His Ser Tyr Val Val 165 170 175		
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Pro Val Tyr Pro Asn Ala Gly Arg Tyr Trp Glu Thr Val Glu Arg Leu 195 200 205		
Lys Ile Asn Gln Phe Tyr Gly Ala Pro Thr Ala Val Arg Leu Leu Leu 210 215 220		
Lys Tyr Gly Asp Ala Trp Val Lys Lys Tyr Asp Arg Ser Ser Leu Arg 225 230 235 240		
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Leu His Arg Val Val Gly Asp Ser Arg Cys Thr Leu Val Asp Thr Trp 260 265 270		
Trp Gln Thr Glu Thr Gly Gly Ile Cys Ile Ala Pro Arg Pro Ser Glu 275 280 285		
Glu Gly Ala Glu Ile Leu Pro Ala Met Ala Met Arg Pro Phe Phe Gly 290 295 300		
Ile Val Pro Val Leu Met Asp Glu Lys Gly Ser Val Val Glu Gly Ser 305 310 315 320		
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Arg Thr Ile Tyr Gly Asp His Gln Arg Phe Val Asp Ala Tyr Phe Lys		

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<211> 1467
<212> DNA
<213> Homo sapiens
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<210> 54

<211> 132

<212> PRT

<213> Homo sapiens

<400> 54

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 35 40 45  
 Ser Ser Ser Leu Gly Pro Thr Leu Ser Cys Leu Ala Cys Cys Leu Gly  
 50 55 60  
 Asp Gln Pro Ser Arg Glu Ala Pro Gly Arg Val Ser Gly Pro Pro Ala  
 65 70 75 80  
 Ile Lys Ala Gly Arg Pro Cys Gly Gln Trp Ala Gln Pro Leu Pro Arg  
 85 90 95  
 Gly Ala Ala Pro Pro Arg Leu Leu Thr Pro Arg Leu Pro Ala Gln Pro  
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 Pro Ala Met Pro Arg Thr Thr Ala Ile Val Pro Trp Gly Ser Pro Ser  
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 Gly Pro Gln Pro  
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<210> 55

<211> 943

<212> DNA

<213> Homo sapiens

<400> 55

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 <211> 86  
 <212> PRT  
 <213> Homo sapiens

<400> 56  
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 Phe Gln Val Phe Leu Tyr Pro Ser Gly Phe Pro Thr Gly Trp Ile Glu  
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<210> 57  
 <211> 1032  
 <212> DNA  
 <213> Homo sapiens

<400> 57  
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<210> 58  
 <211> 71  
 <212> PRT  
 <213> Homo sapiens

&lt;400&gt; 58

Met Phe Leu Ser Leu Pro Thr Leu Thr Val Leu Ile Pro Leu Val Ser  
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Leu Ala Gly Leu Phe Tyr Ser Ala Ser Val Glu Glu Asn Phe Pro Gln  
 20 25 30

Gly Cys Thr Ser Thr Ala Ser Leu Cys Phe Tyr Ser Leu Leu Leu Pro  
 35 40 45

Ile Thr Ile Pro Val Tyr Val Phe Phe His Leu Trp Thr Trp Met Gly  
 50 55 60

Ile Lys Leu Phe Arg His Asn  
 65 70

&lt;210&gt; 59

&lt;211&gt; 1564

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 59

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&lt;210&gt; 60

&lt;211&gt; 82

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 60

Met Val Asn Val Arg Ala Ser Ile Leu Glu Ile Lys Arg His Leu Leu  
 1 5 10 15

Leu His Ser Ser Cys Ala Leu Ser Arg Ser Phe Leu Glu Pro Ser Gly  
                   20                                  25                                  30  
 Ile Gly Leu Trp Asn Cys Thr Leu Met Ser Tyr Leu Ala Pro Ser Trp  
                   35                                  40                                  45  
 Lys Gln Ser Cys Thr Ser Gly Val Val Cys His Pro Pro Ile Ala Ala  
                   50                                  55                                  60  
 Ser Trp Leu Lys Ser Cys Trp Ile Phe Arg Tyr Leu Val Ser Asn Gly  
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Met Tyr

<210> 61

<211> 2800

<212> DNA

<213> Homo sapiens

<400> 61

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&lt;210&gt; 62

&lt;211&gt; 170

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 62

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Met Phe Ser Cys Asn Glu Asn Ser Ile Phe Phe Arg Ile Gly Phe Val
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Phe Ile Leu Leu Ser Phe Ile Ser Ser Cys Gln Thr Leu Asn Gly Tyr
      20             25             30

Val Cys Ile Leu Ile Thr Leu Phe Ser Leu Leu Trp Lys Arg Arg Thr
      35             40             45

Arg Glu Gln Met Leu Leu Arg Ala Gly Val Ser Glu Lys Asn Leu Ser
      50             55             60

Met Leu Phe Asn Val Phe Leu Pro Leu Pro His Ser Val Cys Val Thr
      65             70             75             80

Phe Tyr Asn Ile Lys Lys Tyr Tyr Asn Ile Ser Arg Ile Trp Asn Cys
      85             90             95

His His Asp Glu Trp Pro Phe Gln Cys Ile Val Thr Glu Ile Pro Glu
      100            105            110

Asp Ser Pro Gly Leu Gln Phe His Trp Phe Leu Phe Ala Val Phe Ser
      115            120            125

Cys Cys Asn Cys Cys Cys Phe Gln Ser Lys Gly Pro Pro Leu Val Lys
      130            135            140

Val Asn Lys Thr Ser Pro Leu Cys Tyr Pro Ala Arg Phe Cys Val Cys
      145            150            155            160

Asn Gly Leu Ala Gln Glu Cys Ser Phe Thr
      165            170

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&lt;210&gt; 63

&lt;211&gt; 2056

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 63

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aaaaaaaaaaaa aaaaaa 2056

```

&lt;210&gt; 64

&lt;211&gt; 81

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 64

```

Met Lys Val Pro Thr Ser His His Ser Asp Glu Lys His Gln Glu Ala
  1              5              10              15

```

```

Ser Cys Thr Phe Leu Arg Gly His Ser Arg Ile Asn Pro Pro Leu His
          20              25              30

```

```

Thr Ala Ala Ile Ser Ile Met His His Ser Ile Ser Gly Tyr Met His
    35              40              45

```

```

Asn Arg Val Phe Leu Gly Ala Ser Leu Gly Phe Ser Ser Ser Ala Ile
    50              55              60

```

```

Val Glu Trp Leu His Ser Gln Gly Leu Ala Met Glu Ala His Lys Arg
    65              70              75              80

```

Ala

&lt;210&gt; 65

&lt;211&gt; 581

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 65

```

aaaatatata tgaatagata aatataacta atgtgcgtga gaatgggcct ggcacacctg 60
gggtgctcgg gggtagggct gccatgctgc agagctgatg gagtgatgtt gtgggcacaa 120
ggcatctgtc agctgcctcc tttaacagcc atgccttctg gaatctggaa gaggacacca 180
ctcctgcagt cactgggcag ccacatagca gctgcaggtc ccaggagggc ctgagggtcaa 240
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taaaaagaga cttttctaaa aaaaaaaaaa aaaaaaaaaa a 581

```

&lt;210&gt; 66

&lt;211&gt; 67

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 66

```

Met Cys Val Arg Met Gly Leu Ala His Leu Gly Cys Ser Gly Val Gly
  1             5             10             15

```

```

Leu Pro Cys Cys Arg Ala Asp Gly Val Met Leu Trp Ala Gln Gly Ile
          20             25             30

```

```

Cys Gln Leu Pro Pro Leu Thr Ala Met Pro Ser Gly Ile Trp Lys Arg
          35             40             45

```

```

Thr Pro Leu Leu Gln Ser Leu Gly Ser His Ile Ala Ala Ala Gly Pro
          50             55             60

```

```

Arg Arg Ala
  65

```

&lt;210&gt; 67

&lt;211&gt; 1916

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 67

```

gaaggagaga cggctggcca ccatgcacgg ctectgcagt ttectgatgc ttctgctgcc 60
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```

```

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tgactctcca ataaaaacct gtccaacctg tgaaaaaaaa aaaaaaaa aaaaaa 1916

```

&lt;210&gt; 68

&lt;211&gt; 238

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 68

```

Met His Gly Ser Cys Ser Phe Leu Met Leu Leu Leu Pro Leu Leu Leu
  1              5              10              15

Leu Leu Val Ala Thr Thr Gly Pro Val Gly Ala Leu Thr Asp Glu Glu
          20              25              30

Lys Arg Leu Met Val Glu Leu His Asn Leu Tyr Arg Ala Gln Val Ser
  35              40              45

Pro Thr Ala Ser Asp Met Leu His Met Arg Trp Asp Glu Glu Leu Ala
  50              55              60

Ala Phe Ala Lys Ala Tyr Ala Arg Gln Cys Val Trp Gly His Asn Lys
  65              70              75              80

Glu Arg Gly Arg Arg Gly Glu Asn Leu Phe Ala Ile Thr Asp Glu Glu
          85              90              95

Pro Val Thr Phe Pro Lys Ser Thr His Val Pro Ile Pro Lys Ser Ala
  100             105             110

Asp Lys Val Thr Asp Lys Thr Lys Val Pro Ser Arg Ser Pro Glu Asn
  115             120             125

Ser Leu Asp Pro Lys Met Ser Leu Thr Gly Ala Arg Glu Leu Leu Pro
  130             135             140

His Ala Gln Glu Glu Ala Glu Ala Glu Ala Glu Leu Pro Pro Ser Ser
  145             150             155             160

Glu Val Leu Ala Ser Val Phe Pro Ala Gln Asp Lys Pro Gly Glu Leu
          165             170             175

Gln Ala Thr Leu Asp His Thr Gly His Thr Ser Ser Lys Ser Leu Pro
  180             185             190

Asn Phe Pro Asn Thr Ser Ala Thr Ala Asn Ala Thr Gly Gly Arg Ala
  195             200             205

```

Leu Ala Leu Gln Ser Ser Leu Pro Gly Lys Ala His Ser Ile Cys Pro  
 210 215 220

Thr Phe Leu Leu Ala Leu Glu Cys Gln Tyr Pro Ala Pro Ala  
 225 230 235

<210> 69  
 <211> 2051  
 <212> DNA  
 <213> Homo sapiens

<400> 69  
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 aaaaaaaaaa a 2051

<210> 70  
 <211> 432  
 <212> PRT  
 <213> Homo sapiens

<400> 70  
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Leu Gly Ala Gly Gly Glu Thr Pro Glu Ala Pro Pro Glu Ser Trp Thr  
 20 25 30

Gln Leu Trp Phe Phe Arg Phe Val Val Asn Ala Ala Gly Tyr Ala Ser  
 35 40 45  
 Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Phe Arg Arg Lys Asn  
 50 55 60  
 Tyr Leu Glu Thr Gly Arg Gly Leu Cys Phe Pro Leu Val Lys Ala Cys  
 65 70 75 80  
 Val Phe Gly Asn Glu Pro Lys Ala Ser Asp Glu Val Pro Leu Ala Pro  
 85 90 95  
 Arg Thr Glu Ala Ala Glu Thr Thr Pro Met Trp Gln Ala Leu Lys Leu  
 100 105 110  
 Leu Phe Cys Ala Thr Gly Leu Gln Val Ser Tyr Leu Thr Trp Gly Val  
 115 120 125  
 Leu Gln Glu Arg Val Met Thr Arg Ser Tyr Gly Ala Thr Ala Thr Ser  
 130 135 140  
 Pro Gly Glu Arg Phe Thr Asp Ser Gln Phe Leu Val Leu Met Asn Arg  
 145 150 155 160  
 Val Leu Ala Leu Ile Val Ala Gly Leu Ser Cys Val Leu Cys Lys Gln  
 165 170 175  
 Pro Arg His Gly Ala Pro Met Tyr Arg Tyr Ser Phe Ala Ser Leu Ser  
 180 185 190  
 Asn Val Leu Ser Ser Trp Cys Gln Tyr Glu Ala Leu Lys Phe Val Ser  
 195 200 205  
 Phe Pro Thr Gln Val Leu Ala Lys Ala Ser Lys Val Ile Pro Val Met  
 210 215 220  
 Leu Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu His Trp Glu Tyr  
 225 230 235 240  
 Leu Thr Ala Thr Leu Ile Ser Ile Gly Val Ser Met Phe Leu Leu Ser  
 245 250 255  
 Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu  
 260 265 270  
 Ile Leu Leu Ala Gly Tyr Ile Ala Phe Asp Ser Phe Thr Ser Asn Trp  
 275 280 285  
 Gln Asp Ala Leu Phe Ala Tyr Lys Met Ser Ser Val Gln Met Met Phe  
 290 295 300  
 Gly Val Asn Phe Phe Ser Cys Leu Phe Thr Val Gly Ser Leu Leu Glu  
 305 310 315 320  
 Gln Gly Ala Leu Leu Glu Gly Thr Arg Phe Met Gly Arg His Ser Glu  
 325 330 335  
 Phe Ala Ala His Ala Leu Leu Leu Ser Ile Cys Ser Ala Cys Gly Gln  
 340 345 350

Leu Phe Ile Phe Tyr Thr Ile Gly Gln Phe Gly Ala Ala Val Phe Thr  
 355 360 365

Ile Ile Met Thr Leu Arg Gln Ala Phe Ala Ile Leu Leu Ser Cys Leu  
 370 375 380

Leu Tyr Gly His Thr Val Thr Val Val Gly Gly Leu Gly Val Ala Val  
 385 390 395 400

Val Phe Ala Ala Leu Leu Arg Val Tyr Ala Arg Gly Arg Leu Lys  
 405 410 415

Gln Arg Gly Lys Lys Ala Val Pro Val Glu Ser Pro Val Gln Lys Val  
 420 425 430

<210> 71

<211> 2557

<212> DNA

<213> Homo sapiens

<400> 71

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 tcattactga ggctctgtac gggccaaagt acaccttctt caacaatgtt ttgatgtttt 180  
 cccagctgt gtcaaagagc tgctttttct cctgggtggg tcaggtcaca gaagactgct 240  
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```

&lt;210&gt; 72

&lt;211&gt; 474

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 72

```

Met Phe Ser Pro Ala Val Ser Lys Ser Cys Phe Ser Pro Trp Val Gly
  1           5           10          15

```

```

Gln Val Thr Glu Asp Cys Ser Ser Lys Trp Ser Lys Tyr Lys His Asp
      20           25           30

```

```

Leu Ala Ala Ser Cys Gln Gly Arg Val Val Ala Ala Glu Glu Lys Asn
    35           40           45

```

```

Gly Val Val Phe Ile Arg Gly Glu Gly Val Gly Ala Tyr Asn Pro Gln
    50           55           60

```

```

Leu Asn Leu Lys Asn Val Gln Arg Asn Leu Ile Leu Leu His Pro Gln
    65           70           75           80

```

```

Leu Leu Leu Leu Val Asp Gln Ile His Leu Gly Glu Glu Ser Pro Leu
      85           90           95

```

```

Glu Thr Ala Ala Ser Phe Phe His Asn Val Asp Val Pro Phe Glu Glu
    100          105          110

```

```

Thr Val Val Asp Gly Val His Gly Ala Phe Ile Arg Gln Arg Asp Gly
    115          120          125

```

```

Leu Tyr Lys Met Tyr Trp Met Asp Asp Thr Gly Tyr Ser Glu Lys Ala
    130          135          140

```

```

Thr Phe Ala Ser Val Thr Tyr Pro Arg Gly Tyr Pro Tyr Asn Gly Thr
    145          150          155          160

```

```

Asn Tyr Val Asn Val Thr Met His Leu Arg Ser Pro Ile Thr Arg Ala
    165          170          175

```

```

Ala Tyr Leu Phe Ile Gly Pro Ser Ile Asp Val Gln Ser Phe Thr Val
    180          185          190

```

```

His Gly Asp Ser Gln Gln Leu Asp Val Phe Ile Ala Thr Ser Lys His
    195          200          205

```

```

Ala Tyr Ala Thr Tyr Leu Trp Thr Gly Glu Ala Thr Gly Gln Ser Ala
    210          215          220

```

```

Phe Ala Gln Val Ile Ala Asp Arg His Lys Ile Leu Phe Asp Arg Asn
    225          230          235          240

```

```

Ser Ala Ile Lys Ser Ser Ile Val Pro Glu Val Lys Asp Tyr Ala Ala
    245          250          255

```



Ile Val Glu Gln Asn Leu Gln His Phe Lys Pro Val Phe Gln Leu Leu  
 260 265 270  
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 Thr Ala Glu Arg Leu Leu Arg Phe Ser Asp Lys Arg Gln Thr Glu Glu  
 290 295 300  
 Ala Ile Asp Arg Ile Phe Ala Ile Ser Gln Gln Gln Gln Gln Ser  
 305 310 315 320  
 Lys Ser Lys Lys Asn Arg Arg Ala Gly Lys Arg Tyr Lys Phe Val Asp  
 325 330 335  
 Ala Val Pro Asp Ile Phe Ala Gln Ile Glu Val Asn Glu Lys Lys Ile  
 340 345 350  
 Arg Gln Lys Ala Gln Ile Leu Ala Gln Lys Glu Leu Pro Ile Asp Glu  
 355 360 365  
 Asp Glu Glu Met Lys Asp Leu Leu Asp Phe Ala Asp Val Thr Tyr Glu  
 370 375 380  
 Lys His Lys Asn Gly Gly Leu Ile Lys Gly Arg Phe Gly Gln Ala Arg  
 385 390 395 400  
 Met Val Thr Thr Thr His Ser Arg Ala Pro Ser Leu Ser Ala Ser Tyr  
 405 410 415  
 Thr Arg Leu Phe Leu Ile Leu Asn Ile Ala Ile Phe Phe Val Met Leu  
 420 425 430  
 Ala Met Gln Leu Thr Tyr Phe Gln Arg Ala Gln Ser Leu His Gly Gln  
 435 440 445  
 Arg Cys Leu Tyr Ala Val Leu Leu Ile Asp Ser Cys Ile Leu Leu Trp  
 450 455 460  
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<210> 73  
 <211> 3442  
 <212> DNA  
 <213> Homo sapiens

<400> 73  
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&lt;210&gt; 74

&lt;211&gt; 61

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 74

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Met Lys Lys His Arg Arg Ala Leu Ala Leu Val Ser Cys Leu Phe Leu
1           5           10          15

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Cys Ser Leu Val Trp Leu Pro Ser Trp Arg Val Cys Cys Lys Glu Ser
20          25          30

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Ser Ser Ala Ser Ala Ser Ser Tyr Tyr Ser Gln Asp Asp Asn Cys Ala  
 35 40 45

Leu Glu Asn Glu Asp Val Gln Phe Gln Lys Lys Val Pro  
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<210> 75

<211> 1159

<212> DNA

<213> Homo sapiens

<400> 75

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<210> 76

<211> 242

<212> PRT

<213> Homo sapiens

<400> 76

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 20 25 30

Gly Ser Gly Gly Ser Gly Val Gly Ile Gly Asp Arg Phe Lys Ile Glu  
 35 40 45

Gly Arg Ala Val Val Pro Gly Val Lys Pro Gln Asp Trp Ile Ser Ala  
 50 55 60

Ala Arg Val Leu Val Asp Gly Glu Glu His Val Gly Phe Leu Lys Thr  
 65 70 75 80

Asp Gly Ser Phe Val Val His Asp Ile Pro Ser Gly Ser Tyr Val Val  
 85 90 95

Glu Val Val Ser Pro Ala Tyr Arg Phe Asp Pro Val Arg Val Asp Ile

100	105	110
Thr Ser Lys Gly Lys Met Arg Ala Arg Tyr Val Asn Tyr Ile Lys Thr		
115	120	125
Ser Glu Val Val Arg Leu Pro Tyr Pro Leu Gln Met Lys Ser Ser Gly		
130	135	140
Pro Pro Ser Tyr Phe Ile Lys Arg Glu Ser Trp Gly Trp Thr Asp Phe		
145	150	155
Leu Met Asn Pro Met Val Met Met Met Val Leu Pro Leu Leu Ile Phe		
165	170	175
Val Leu Leu Pro Lys Val Val Asn Thr Ser Asp Pro Asp Met Arg Arg		
180	185	190
Glu Met Glu Gln Ser Met Asn Met Leu Asn Ser Asn His Glu Leu Pro		
195	200	205
Asp Val Ser Glu Phe Met Thr Arg Leu Phe Ser Ser Lys Ser Ser Gly		
210	215	220
Lys Ser Ser Ser Gly Ser Ser Lys Thr Gly Lys Ser Gly Ala Gly Lys		
225	230	235
		240
Arg Arg		

&lt;210&gt; 77

&lt;211&gt; 2462

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 77

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&lt;210&gt; 78

&lt;211&gt; 94

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 78

Met Ala Ser Val Val Leu Ala Leu Arg Thr Arg Thr Ala Val Thr Ser  
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 Leu Leu Ser Pro Thr Pro Ala Thr Ala Leu Ala Val Arg Tyr Ala Ser  
 20 25 30  
 Lys Lys Ser Gly Gly Ser Ser Lys Asn Leu Gly Gly Lys Ser Ser Gly  
 35 40 45  
 Arg Arg Gln Gly Ile Lys Lys Met Glu Gly His Tyr Val His Ala Gly  
 50 55 60  
 Asn Ile Ile Ala Thr Gln Arg His Phe Arg Trp His Pro Gly Ala His  
 65 70 75 80  
 Val Ser Cys Ser Val Ala Ala Pro Leu Phe Pro Phe Leu Gly  
 85 90

&lt;210&gt; 79

&lt;211&gt; 1178

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 79

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<210> 80  
 <211> 62  
 <212> PRT  
 <213> Homo sapiens

<400> 80  
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 20 25 30  
 Ser Met Thr Thr Leu Glu Asp Val Phe Leu Lys Leu Glu Val Glu Ala  
 35 40 45  
 Glu Ile Asp Gln Ala Gly Lys Asn Arg Thr Asn Lys Thr Phe  
 50 55 60

<210> 81  
 <211> 1285  
 <212> DNA  
 <213> Homo sapiens

<400> 81  
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<210> 82

<211> 61  
 <212> PRT  
 <213> Homo sapiens

<400> 82  
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                   20                  25                  30  
 Lys Gln Leu Cys Gln Lys Leu Tyr Ser Ser Lys Asp Thr Thr Lys Arg  
           35                  40                  45  
 Pro Val Thr Thr Thr Lys Arg Glu Val Asn Ser Ala Ile  
           50                  55                  60

<210> 83  
 <211> 654  
 <212> DNA  
 <213> Homo sapiens

<400> 83  
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<210> 84  
 <211> 119  
 <212> PRT  
 <213> Homo sapiens

<400> 84  
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                   20                  25                  30  
 Arg Asp Arg Gly Gln Ala Ser Arg Arg Trp Leu Gln Glu Gly Gly Gln  
           35                  40                  45  
 Glu Cys Glu Cys Lys Asp Trp Phe Leu Arg Ala Pro Arg Arg Lys Phe  
           50                  55                  60  
 Met Thr Val Ser Gly Leu Pro Lys Lys Gln Cys Pro Cys Asp His Phe  
           65                  70                  75                  80  
 Lys Gly Asn Val Lys Lys Thr Arg His Gln Arg His His Arg Lys Pro  
                   85                  90                  95

Asn Lys His Ser Arg Ala Cys Gln Gln Phe Leu Lys Gln Cys Gln Leu  
 100 105 110

Arg Ser Phe Ala Leu Pro Leu  
 115

<210> 85  
 <211> 1176  
 <212> DNA  
 <213> Homo sapiens

<400> 85  
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<210> 86  
 <211> 78  
 <212> PRT  
 <213> Homo sapiens

<400> 86  
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<210> 87  
 <211> 1476  
 <212> DNA  
 <213> Homo sapiens



&lt;400&gt; 87

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&lt;210&gt; 88

&lt;211&gt; 145

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 88

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 Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln  
 35 40 45  
 Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly  
 50 55 60  
 Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn  
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Gly  
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<210> 89  
<211> 2243  
<212> DNA  
<213> Homo sapiens

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<210> 90  
<211> 61  
<212> PRT  
<213> Homo sapiens

<400> 90  
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20

25

30

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<210> 91  
<211> 1041  
<212> DNA  
<213> Homo sapiens

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<210> 92  
<211> 228  
<212> PRT  
<213> Homo sapiens

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35 40 45  
Leu Val Ala Cys Asn Ile Leu Cys Leu Leu Val Asp Glu Thr Ala Met  
50 55 60  
Pro Lys Gly Thr Arg Gly Pro Gly Ile Gly Asn Ala Ser Leu Ser Thr  
65 70 75 80  
Phe Gly Phe Val Gly Ala Ala Leu Glu Ile Ile Leu Ile Phe Tyr Leu  
85 90 95  
Met Val Ser Ser Val Val Gly Phe Tyr Ser Leu Arg Phe Phe Gly Asn  
100 105 110

Phe Thr Pro Lys Lys Asp Asp Thr Thr Met Thr Lys Ile Ile Gly Asn  
115 120 125

Cys Val Ser Ile Leu Val Leu Ser Ser Ala Leu Pro Val Met Ser Arg  
130 135 140

Thr Leu Gly Ile Thr Arg Phe Asp Leu Leu Gly Asp Phe Gly Arg Phe  
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Asn Trp Leu Gly Asn Phe Tyr Ile Val Leu Ser Tyr Asn Leu Leu Phe  
165 170 175

Ala Ile Val Thr Thr Leu Cys Leu Val Arg Lys Phe Thr Ser Ala Val  
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Arg Glu Glu Leu Phe Lys Ala Leu Gly Leu His Lys Leu His Leu Pro  
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Asn Thr Ser Arg Asp Ser Glu Thr Ala Lys Pro Ser Val Asn Gly His  
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Gln Lys Ala Leu  
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<210> 93

<211> 1792

<212> DNA

<213> Homo sapiens

<400> 93

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<210> 94  
 <211> 254  
 <212> PRT  
 <213> Homo sapiens

<400> 94  
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 Ser Val Thr Gly Ser Cys Tyr Cys Gly Lys Arg Ile Ser Ser Asp Ser  
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 Pro Pro Ser Val Gln Phe Met Asn Arg Leu Arg Lys His Leu Arg Ala  
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 Tyr His Arg Cys Leu Tyr Tyr Thr Arg Phe Gln Leu Leu Ser Trp Ser  
 65 70 75 80  
 Val Cys Gly Gly Asn Lys Asp Pro Trp Val Gln Glu Leu Met Ser Cys  
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 Leu Asp Leu Lys Glu Cys Gly His Ala Tyr Ser Gly Ile Val Ala His  
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 Gln Lys His Leu Leu Pro Thr Ser Pro Pro Thr Ser Gln Ala Ser Glu  
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 Gly Ala Ser Ser Asp Ile His Thr Pro Ala Gln Met Leu Leu Ser Thr  
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 Leu Gln Ser Thr Gln Arg Pro Thr Leu Pro Val Gly Ser Leu Ser Ser  
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 Asp Lys Glu Leu Thr Arg Pro Asn Glu Thr Thr Ile His Thr Ala Gly  
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 His Ser Leu Ala Val Gly Pro Glu Ala Gly Glu Asn Gln Lys Gln Pro  
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 Glu Lys Asn Ala Gly Pro Thr Ala Arg Thr Ser Ala Thr Val Pro Val  
 195 200 205  
 Leu Cys Leu Leu Ala Ile Ile Phe Ile Leu Thr Ala Ala Leu Ser Tyr  
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 Val Leu Cys Lys Arg Arg Arg Gly Gln Ser Pro Gln Ser Ser Pro Asp  
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<210> 95  
 <211> 1234

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 95

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&lt;210&gt; 96

&lt;211&gt; 229

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 96

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Asp Ser Asp Phe Thr Phe Thr Leu Pro Ala Gly Gln Lys Glu Cys Phe
  35              40              45

Tyr Gln Pro Met Pro Leu Lys Ala Ser Leu Glu Ile Glu Tyr Gln Val
  50              55              60

Leu Asp Gly Ala Gly Leu Asp Ile Asp Phe His Leu Ala Ser Pro Glu
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Gly Lys Thr Leu Val Phe Glu Gln Arg Lys Ser Asp Gly Val His Thr
  85              90              95

Val Glu Thr Glu Val Gly Asp Tyr Met Phe Cys Phe Asp Asn Thr Phe
 100              105              110

Ser Thr Ile Ser Glu Lys Val Ile Phe Phe Glu Leu Ile Leu Asp Asn
 115              120              125

Met Gly Glu Gln Ala Gln Glu Gln Glu Asp Trp Lys Lys Tyr Ile Thr
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Gly Thr Asp Ile Leu Asp Met Lys Leu Glu Asp Ile Leu Glu Ser Ile

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<212> DNA
<213> Homo sapiens
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<210> 98
<211> 92
<212> PRT
<213> Homo sapiens
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<400> 98
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Ile Ser Leu Cys Leu Thr Leu Leu Ser Val Thr Pro Asp Ile Leu Gln
      20              25              30

Pro Gly Gly Thr Phe Leu Cys Lys Thr Trp Ala Gly Ser Gln Ser Arg
    35              40              45

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Arg Leu Gln Arg Arg Leu Thr Glu Glu Phe Gln Asn Val Arg Ile Ile  
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Lys Pro Glu Ala Ser Arg Lys Glu Ser Ser Glu Val Tyr Phe Leu Ala  
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Thr Gln Tyr His Gly Arg Lys Gly Thr Val Lys Gln  
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<210> 99  
<211> 1343  
<212> DNA  
<213> Homo sapiens

<400> 99  
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aggccatgag aggaagggga gga 1343

<210> 100  
<211> 210  
<212> PRT  
<213> Homo sapiens

<400> 100  
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Pro Ala Leu Gly Ser Arg Ile Ala Gly Ile Thr Gly Lys His His His  
20 25 30  
Leu Trp Leu Ile Phe Ile Phe Leu Val Glu Thr Gly Phe His His Val  
35 40 45  
Gly His Ala Ser Ile Ser Ser Phe Leu Ile Thr Asp Lys Ser Arg Pro  
50 55 60  
Lys Ile Ser Gly Thr Arg Tyr His Gln Val Arg Leu Pro Thr Phe Val



65		70		75		80
Cys Phe Pro Leu Phe Met Ser Cys Phe Leu Ala Trp Lys Leu Thr Ser						
	85		90		95	
Lys Leu Tyr Asn Ser Asp Leu Lys Thr Gly Lys Tyr Ser Glu His Ser						
	100		105		110	
Ile Ser Thr Gly Ser Thr Phe Val Asp Ser Thr Asn Tyr Arg Leu Lys						
	115		120		125	
Ile Phe Gly Lys Ile Lys Arg Ile Val Val Phe Val Leu Asn Met Asn						
	130		135		140	
Arg Phe Leu Phe Cys His His Phe Leu Asn Asn Thr Thr Ala Met Tyr						
	145		150		155	160
Thr Gln Tyr Leu Ser Ser Phe Thr Lys Ile Thr Cys Ala Ser Arg Ala						
	165		170		175	
Pro Phe Ser Tyr Gln Ser His Leu His Val Val Val Leu Phe Gln Leu						
	180		185		190	
Glu Asn Lys Thr Gly Val Leu Cys Ala Val Asn Gln Thr Lys Leu Phe						
	195		200		205	
Met Gln						
210						

&lt;210&gt; 101

&lt;211&gt; 1529

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 101

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<210> 102  
 <211> 75  
 <212> PRT  
 <213> Homo sapiens

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 Val Asp Gln Ser Arg Asn Tyr Ile Ser Asn Ser Ala Gln Ser Asn Gly  
 35 40 45  
 Ala Val Val Lys Glu Lys Ala Pro Ala Ala Pro Lys Thr Pro Ser Lys  
 50 55 60  
 Ala Lys Lys Asn Lys Asp Lys Glu Tyr Tyr Val  
 65 70 75

<210> 103  
 <211> 733  
 <212> DNA  
 <213> Homo sapiens

<400> 103  
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<210> 104  
 <211> 52  
 <212> PRT  
 <213> Homo sapiens

<400> 104  
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 1 5 10 15  
 Leu Phe Gly Pro His Ile Leu His Phe Ala Leu Ser Ser Arg Val Gln  
 20 25 30  
 Trp Lys Gly Asn Lys Asn Thr Asp Tyr Ser Glu Gln Phe Ser Pro Lys  
 35 40 45

Arg Ile Ala Phe

50

&lt;210&gt; 105

&lt;211&gt; 2342

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 105

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aa

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&lt;210&gt; 106

&lt;211&gt; 431

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 106

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1

5

10

15

Cys Phe Leu Thr Leu Arg Leu Ser Ala Ser Gln Asn Cys Leu Lys Lys  
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 Ser Leu Glu Asp Val Val Ile Asp Ile Gln Ser Ser Leu Ser Lys Gly  
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 Ile Arg Gly Asn Glu Pro Val Tyr Thr Ser Thr Gln Glu Asp Cys Ile  
 50 55 60  
 Asn Ser Cys Cys Ser Thr Lys Asn Ile Ser Gly Asp Lys Ala Cys Asn  
 65 70 75 80  
 Leu Met Ile Phe Asp Thr Arg Lys Thr Ala Arg Gln Pro Asn Cys Tyr  
 85 90 95  
 Leu Phe Phe Cys Pro Asn Glu Glu Ala Cys Pro Leu Lys Pro Ala Lys  
 100 105 110  
 Gly Leu Met Ser Tyr Arg Ile Ile Thr Asp Phe Pro Ser Leu Thr Arg  
 115 120 125  
 Asn Leu Pro Ser Gln Glu Leu Pro Gln Glu Asp Ser Leu Leu His Gly  
 130 135 140  
 Gln Phe Ser Gln Ala Val Thr Pro Leu Ala His His His Thr Asp Tyr  
 145 150 155 160  
 Ser Lys Pro Thr Asp Ile Ser Trp Arg Asp Thr Leu Ser Gln Lys Phe  
 165 170 175  
 Gly Ser Ser Asp His Leu Glu Lys Leu Phe Lys Met Asp Glu Ala Ser  
 180 185 190  
 Ala Gln Leu Leu Ala Tyr Lys Glu Lys Gly His Ser Gln Ser Ser Gln  
 195 200 205  
 Phe Ser Ser Asp Gln Glu Ile Ala His Leu Leu Pro Glu Asn Val Ser  
 210 215 220  
 Ala Leu Pro Ala Thr Val Ala Val Ala Ser Pro His Thr Thr Ser Ala  
 225 230 235 240  
 Thr Pro Lys Pro Ala Thr Leu Leu Pro Thr Asn Ala Ser Val Thr Pro  
 245 250 255  
 Ser Gly Thr Ser Gln Pro Gln Leu Ala Thr Thr Ala Pro Pro Val Thr  
 260 265 270  
 Thr Val Thr Ser Gln Pro Pro Thr Thr Leu Ile Ser Thr Val Phe Thr  
 275 280 285  
 Arg Ala Ala Ala Thr Leu Gln Ala Met Ala Thr Thr Ala Val Leu Thr  
 290 295 300  
 Thr Thr Phe Gln Ala Pro Thr Asp Ser Lys Gly Ser Leu Glu Thr Ile  
 305 310 315 320  
 Pro Phe Thr Glu Ile Ser Asn Leu Thr Leu Asn Thr Gly Asn Val Tyr  
 325 330 335

Asn Pro Thr Ala Leu Ser Met Ser Asn Val Glu Ser Ser Thr Met Asn  
 340 345 350

Lys Thr Ala Ser Trp Glu Gly Arg Glu Ala Ser Pro Gly Ser Ser Ser  
 355 360 365

Gln Gly Ser Val Pro Glu Asn Gln Tyr Gly Leu Pro Phe Glu Lys Trp  
 370 375 380

Leu Leu Ile Gly Ser Leu Leu Phe Gly Val Leu Phe Leu Val Ile Gly  
 385 390 395 400

Leu Val Leu Leu Gly Arg Ile Leu Ser Glu Ser Leu Arg Arg Lys Arg  
 405 410 415

Tyr Ser Arg Leu Asp Tyr Leu Ile Asn Gly Ile Tyr Val Asp Ile  
 420 425 430

<210> 107

<211> 3153

<212> DNA

<213> Homo sapiens

<400> 107

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&lt;210&gt; 108

&lt;211&gt; 102

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 108

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Met Glu Leu Val Arg Arg Leu Met Pro Leu Thr Leu Leu Ile Leu Ser
  1                      5                      10                      15

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Cys Leu Ala Glu Leu Thr Met Ala Glu Ala Glu Gly Asn Ala Ser Cys
          20                      25                      30

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Thr Val Ser Leu Gly Gly Ala Asn Met Ala Glu Thr His Lys Ala Met
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Ile Leu Gln Leu Asn Pro Ser Glu Asn Cys Thr Trp Thr Ile Glu Arg
      50                      55                      60

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Pro Glu Asn Lys Ala Ser Glu Leu Ser Phe Pro Met Ser Ser Leu Ile
      65                      70                      75                      80

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Gln Met Glu Ala Val Lys Val Lys Thr Leu Lys Ser Leu Thr Glu Pro
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Pro Ala Met Gly Leu Cys
          100

```

&lt;210&gt; 109

&lt;211&gt; 1805

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 109

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aaaaa 1805

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&lt;210&gt; 110

&lt;211&gt; 406

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 110

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Gly Pro Leu Gln Gly Gln Gln His His Leu Val Glu Tyr Met Glu Arg
 20              25              30

Arg Leu Ala Ala Leu Glu Glu Arg Leu Ala Gln Cys Gln Asp Gln Ser
 35              40              45

Ser Arg His Ala Ala Glu Leu Arg Asp Phe Lys Asn Lys Met Leu Pro
 50              55              60

Leu Leu Glu Val Ala Glu Lys Glu Arg Glu Ala Leu Arg Thr Glu Ala
 65              70              75              80

Asp Thr Ile Ser Gly Arg Val Asp Arg Leu Glu Arg Glu Val Asp Tyr
 85              90              95

Leu Glu Thr Gln Asn Pro Ala Leu Pro Cys Val Glu Phe Asp Glu Lys
100              105              110

Val Thr Gly Gly Pro Gly Thr Lys Gly Lys Gly Arg Arg Asn Glu Lys
115              120              125

Tyr Asp Met Val Thr Asp Cys Gly Tyr Thr Ile Ser Gln Val Arg Ser
130              135              140

Met Lys Ile Leu Lys Arg Phe Gly Gly Pro Ala Gly Leu Trp Thr Lys
145              150              155              160

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 Met Ala Ala Arg Lys Ala Ser Arg Val Arg Val Pro Phe Pro Trp Val  
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 Gly Thr Gly Gln Leu Val Tyr Gly Gly Phe Leu Tyr Phe Ala Arg Arg  
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 Pro Pro Gly Arg Pro Gly Gly Gly Gly Glu Met Glu Asn Thr Leu Gln  
 225 230 235 240  
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 245 250 255  
 Phe Pro Ala Glu Gly Leu Ile Pro Pro Tyr Gly Leu Thr Ala Asp Thr  
 260 265 270  
 Tyr Ile Asp Leu Ala Ala Asp Glu Glu Gly Leu Trp Ala Val Tyr Ala  
 275 280 285  
 Thr Arg Glu Asp Asp Arg His Leu Cys Leu Ala Lys Leu Asp Pro Gln  
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 Thr Leu Asp Thr Glu Gln Gln Trp Asp Thr Pro Cys Pro Arg Glu Asn  
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 Thr Arg Pro Ala Ser Arg Ala Arg Ile Gln Cys Ser Phe Asp Ala Ser  
 340 345 350  
 Gly Thr Leu Thr Pro Glu Arg Ala Ala Leu Pro Tyr Phe Pro Arg Arg  
 355 360 365  
 Tyr Gly Ala His Ala Ser Leu Arg Tyr Asn Pro Arg Glu Arg Gln Leu  
 370 375 380  
 Tyr Ala Trp Asp Asp Gly Tyr Gln Ile Val Tyr Lys Leu Glu Met Arg  
 385 390 395 400  
 Lys Lys Glu Glu Glu Val  
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&lt;210&gt; 111

&lt;211&gt; 2824

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 111

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&lt;210&gt; 112

&lt;211&gt; 399

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 112

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Met Leu Leu Leu Leu Gly Leu Cys Leu Gly Leu Ser Leu Cys Val Gly
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Ser Gln Glu Glu Ala Gln Ser Trp Gly His Ser Ser Glu Gln Asp Gly
          20                      25                     30

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Leu Arg Val Pro Arg Gln Val Arg Leu Leu Gln Arg Leu Lys Thr Lys
  35                      40                     45

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Pro Leu Met Thr Glu Phe Ser Val Lys Ser Thr Ile Ile Ser Arg Tyr  
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 Glu Arg Glu Lys Lys Ser Gly Asp Arg Val Lys Glu Lys Arg Asn Lys  
 115 120 125  
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 Ala Val Ile Pro Ser Lys Asp Lys Ala Ala Phe Phe Leu Ser Tyr Glu  
 145 150 155 160  
 Glu Leu Leu Gln Arg Arg Leu Gly Lys Tyr Glu His Ser Ile Ser Val  
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 Arg Pro Gln Gln Leu Ser Gly Arg Leu Ser Val Asp Val Asn Ile Leu  
 180 185 190  
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 195 200 205  
 Arg Gln Arg Gly Ser Gly Arg Gly Glu Asp Asp Ser Gly Pro Pro Pro  
 210 215 220  
 Ser Thr Val Ile Asn Gln Asn Glu Thr Phe Ala Asn Ile Ile Phe Lys  
 225 230 235 240  
 Pro Thr Val Val Gln Gln Ala Arg Ile Ala Gln Asn Gly Ile Leu Gly  
 245 250 255  
 Asp Phe Ile Ile Arg Tyr Asp Val Asn Arg Glu Gln Ser Ile Gly Asp  
 260 265 270  
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 275 280 285  
 Leu Pro Pro Leu Pro Lys Asn Val Val Phe Val Leu Asp Ser Ser Ala  
 290 295 300  
 Ser Met Val Gly Thr Lys Leu Arg Gln Thr Lys Asp Ala Leu Phe Thr  
 305 310 315 320  
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 325 330 335  
 Ser Asn Arg Ile Lys Val Trp Lys Asp His Leu Ile Ser Val Thr Pro  
 340 345 350  
 Asp Ser Ile Arg Asp Gly Lys Val Tyr Ile His His Met Ser Pro Thr  
 355 360 365

Gly Gly Lys Asp Asp Thr Phe Phe Ser His Trp Leu Gly Phe Glu Ile  
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 <211> 1711  
 <212> DNA  
 <213> Homo sapiens

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<210> 114  
 <211> 76  
 <212> PRT  
 <213> Homo sapiens

<400> 114  
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 Ala Phe Phe Phe Leu Phe Gly Gln Phe Leu Phe Ile Cys Ala His Asn  
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 Arg Gly Gly Glu Thr Arg Ser Thr Leu Gly Pro Ser Gln Arg Cys Trp  
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Ala Gly Pro Val Ser Arg Pro Gln Leu Leu Lys Leu  
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<210> 115  
 <211> 2116  
 <212> DNA  
 <213> Homo sapiens

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<210> 116  
 <211> 359  
 <212> PRT  
 <213> Homo sapiens

<400> 116  
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Leu Gln Cys Glu Gly Pro Val Cys Thr Glu Glu Ser Ser Cys His Thr  
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 Tyr Thr Phe Ser Glu Pro Phe His Leu Ile Val Ser Tyr Asp Trp Leu  
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 Tyr Arg Asp Gly Ser Ala Leu Gly Pro Pro Gly Pro Asn Arg Glu Phe  
 115 120 125  
 Ser Ile Thr Val Val Gln Lys Ala Asp Ser Gly His Tyr His Cys Ser  
 130 135 140  
 Gly Ile Phe Gln Ser Pro Gly Pro Gly Ile Pro Glu Thr Ala Ser Val  
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 Val Ala Ile Thr Val Gln Glu Leu Phe Pro Ala Pro Ile Leu Arg Ala  
 165 170 175  
 Val Pro Ser Ala Glu Pro Gln Ala Gly Gly Pro Met Thr Leu Ser Cys  
 180 185 190  
 Gln Thr Lys Leu Pro Leu Gln Arg Ser Ala Ala Arg Leu Leu Phe Ser  
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 Phe Tyr Lys Asp Gly Arg Ile Val Gln Ser Arg Gly Leu Ser Ser Glu  
 210 215 220  
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 225 230 235 240  
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 245 250 255  
 Glu Ile Arg Val Gln Gly Ala Ser Ser Ser Ala Ala Pro Pro Thr Leu  
 260 265 270  
 Asn Pro Ala Pro Gln Lys Ser Ala Ala Pro Gly Thr Ala Pro Glu Glu  
 275 280 285  
 Ala Pro Gly Pro Leu Pro Pro Pro Pro Thr Pro Ser Ser Glu Asp Pro  
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 Gly Phe Ser Ser Pro Leu Gly Met Pro Asp Pro His Leu Tyr His Gln  
 305 310 315 320  
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<211> 1391  
<212> DNA  
<213> Homo sapiens

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cccaggtgcc cggaagcagc ctcttcgcat aggcagtgat ttgcgattac tttaaagctc 1260  
accttttttc ttccccctc tgttcgtgc tgtcagcata atgatttgtt tcttcccta 1320  
tgggatccat ctgttttgta aacaataaag cgtctgaggg agtgtaaaaa aaaaaaaaaa 1380  
aaaaaaaaa a 1391

<210> 118  
<211> 56  
<212> PRT  
<213> Homo sapiens

<400> 118  
Met Val Thr Ser Glu Gly Arg Pro Leu Gly Thr His Leu Pro Thr Ala  
1 5 10 15  
Ala Gln Ala Arg Ala Gln Ala His Leu Leu Val Leu Arg Pro Gln Ile  
20 25 30  
Lys Pro Ser Pro His His Met Ala Ser Asp Arg Phe Leu Pro Ser Arg  
35 40 45  
Lys Phe Cys Gly Cys Ala Val Leu  
50 55

<210> 119  
<211> 21  
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<220>

<223> oligonucleotide

<400> 119

cttccacaga acacaagcca c

21

<210> 120

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<400> 120

acgctcaact ccacctcc

18

<210> 121

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<400> 121

cttggaacat agcaccactc c

21

<210> 122

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<400> 122

ccattccaga cttccctgtc

20

<210> 123

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<400> 123

gatgcagggt gtctcctgg

19

<210> 124

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<400> 124

ctgtggacta cggaaggggtg

20

<210> 125  
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<220>  
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<400> 125  
 gaacagatgg actctcccc 20

<210> 126  
 <211> 19  
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<220>  
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<400> 126  
 tggaggcatt gctatgtgg 19

<210> 127  
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<400> 127  
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<220>  
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<400> 128  
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<210> 129  
 <211> 21  
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<220>  
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<400> 129  
 ggacacaaga agaggagagc a 21

<210> 130  
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 <213> Artificial Sequence



<220>  
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<400> 130  
tcacctcaga tgagtgtggc 20

<210> 131  
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<220>  
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<400> 131  
acagatggat gatctgtgaa c 21

<210> 132  
<211> 21  
<212> DNA  
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<220>  
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<400> 132  
ggagactcac tatgaatccc t 21

<210> 133  
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<212> DNA  
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<220>  
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<400> 133  
tttaaacaca ttccctgact c 21

<210> 134  
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<220>  
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<400> 134  
ccttgacag cacttgacat 20

<210> 135  
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<400> 135  
tgggtctcag ttaccatttg g 21

<210> 136  
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<220>  
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<400> 136  
gtgaattagt gaagagccag c 21

<210> 137  
<211> 21  
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<220>  
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<400> 137  
ttctctgaaa ctgagtcgcc t 21

<210> 138  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
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<400> 138  
tgggagtcgc ttagcctatc 20

<210> 139  
<211> 20  
<212> DNA  
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<400> 139  
agtcacgaat ggcacctggt 20

<210> 140  
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<213> Artificial Sequence

<220>  
<223> oligonucleotide

<400> 140  
cataaaacag ctttccccca 20

<210> 141  
<211> 20  
<212> DNA  
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<220>  
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<400> 141  
aggagtttcc agggcagttt 20

<210> 142  
<211> 21  
<212> DNA  
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<220>  
<223> oligonucleotide

<400> 142  
ggctcagata tagttcaggc a 21

<210> 143  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
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<400> 143  
aggcttatac tacggcgggt 20

<210> 144  
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<220>  
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<400> 144  
gggagggaga gtttgtcctc 20

<210> 145  
<211> 20  
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<400> 145  
gcctcaccct ttggttatga 20

<210> 146  
<211> 21  
<212> DNA  
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<220>  
<223> oligonucleotide

<400> 146

aacaggcact ttgaagtcag c 21

<210> 147  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
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<400> 147  
tggttgaga tgaacatccc 20

<210> 148  
<211> 21  
<212> DNA  
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<220>  
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<400> 148  
cctgaagatc cagcatgact t 21

<210> 149  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
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<400> 149  
ggcaaactgt ctaaaaagtg a 21

<210> 150  
<211> 20  
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<213> Artificial Sequence

<220>  
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<400> 150  
atattgcaaa tgctgcacca 20

<210> 151  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<400> 151  
cagctgcctc ctttaacagc 20

<210> 152  
<211> 20  
<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<400> 152

tcatcacacc atccatcctg

20

<210> 153

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<400> 153

ggatccctag gctctgttcc

20

<210> 154

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<400> 154

tggaaaaccg ttatagaccc a

21

<210> 155

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<400> 155

ggctcaggta aacaaagatt g

21

<210> 156

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<400> 156

aagagatcaa cgtcgggatg

20

<210> 157

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<400> 157  
ggggatttca gtttcagcaa 20

<210> 158  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<400> 158  
tcattcaaca accagaacgt g 21

<210> 159  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<400> 159  
gggctatcac tgtggctatg a 21

<210> 160  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<400> 160  
tttaattgga agagtgggcg 20

<210> 161  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<400> 161  
tacctcacgc ctgtaatccc 20

<210> 162  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<400> 162  
gaggagctat ggacgtctgc 20

<210> 163  
<211> 21

<212> DNA  
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<220>  
<223> oligonucleotide

<400> 163  
agttcattca gccttatata a 21

<210> 164  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<400> 164  
ctaggttctg aagaggggcc 20

<210> 165  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<400> 165  
ctgaggccag ttgtttccat 20

<210> 166  
<211> 21  
<212> DNA  
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<220>  
<223> oligonucleotide

<400> 166  
ggatcagcag gattacttgc a 21

<210> 167  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<400> 167  
ttcacgcatt cttcaagcag 20

<210> 168  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<400> 168  
cctgaaatct ttggccttga

20

<210> 169  
<211> 113  
<212> PRT  
<213> Homo sapiens

<400> 169  
Met Val Leu Thr Leu Trp Cys Asn Leu Cys Ser Arg Ala Ser Ser Trp  
1 5 10 15  
Val Arg Gln Lys His Val Ser Cys Cys Val His Asn Tyr Thr Gln Pro  
20 25 30  
Phe Leu Leu Ile Gln Ser Ser Phe Trp Ala Met Ser Ser Glu Thr Lys  
35 40 45  
Pro Lys Ala Leu Ser Lys Asp Tyr Leu Cys Ile Ser Tyr Arg Ser Pro  
50 55 60  
His Ser Thr Pro Thr His Arg His Ser Ser Asn Ser Ser Tyr Asp Leu  
65 70 75 80  
Pro Val Glu Ala Gln Ala Ser Tyr Leu Asp Ile Lys Ser Leu His Gly  
85 90 95  
Gln Ser Gly Leu Cys Leu Ser Arg Phe Ile Phe His Tyr His Thr Pro  
100 105 110  
Tyr

<210> 170  
<211> 321  
<212> PRT  
<213> Homo sapiens

<400> 170  
Met Ala Val Ser Glu Arg Arg Gly Leu Gly Arg Gly Ser Pro Ala Glu  
1 5 10 15  
Trp Gly Gln Arg Leu Leu Leu Val Leu Leu Leu Gly Gly Cys Ser Gly  
20 25 30  
Arg Ile His Arg Leu Ala Leu Thr Gly Glu Lys Arg Ala Asp Ile Gln  
35 40 45  
Leu Asn Ser Phe Gly Phe Tyr Thr Asn Gly Ser Leu Glu Val Glu Leu  
50 55 60  
Ser Val Leu Arg Leu Gly Leu Arg Glu Ala Glu Glu Lys Ser Leu Leu  
65 70 75 80  
Val Gly Phe Ser Leu Ser Arg Val Arg Ser Gly Arg Val Arg Ser Tyr  
85 90 95  
Ser Thr Arg Asp Phe Gln Asp Cys Pro Leu Gln Lys Asn Ser Ser Ser



100	105	110
Phe Leu Val	Leu Phe Leu Ile Asn Thr Lys Asp Leu Gln Val Gln Val	
115	120	125
Arg Lys Tyr Gly Glu Gln Lys Thr Leu Phe Ile Phe Pro Gly Leu Leu		
130	135	140
Pro Glu Ala Pro Ser Lys Pro Gly Leu Pro Lys Pro Gln Ala Thr Val		
145	150	155
Pro Arg Lys Val Asp Gly Gly Gly Thr Ser Ala Ala Ser Lys Pro Lys		
165	170	175
Ser Thr Pro Ala Val Ile Gln Gly Pro Ser Gly Lys Asp Lys Asp Leu		
180	185	190
Val Leu Gly Leu Ser His Leu Asn Asn Ser Tyr Asn Phe Ser Phe His		
195	200	205
Val Val Ile Gly Ser Gln Ala Glu Glu Gly Gln Tyr Ser Leu Asn Phe		
210	215	220
His Asn Cys Asn Asn Ser Val Pro Gly Lys Glu His Pro Phe Asp Ile		
225	230	235
Thr Val Met Ile Arg Glu Lys Asn Pro Asp Gly Phe Leu Ser Ala Ala		
245	250	255
Glu Met Pro Leu Phe Lys Leu Tyr Met Val Met Ser Ala Cys Phe Leu		
260	265	270
Ala Ala Gly Ser Gly Cys Thr Ser Ser Trp Trp Arg Ala Pro Pro Trp		
275	280	285
Pro Ser Ser Cys Ser Arg Ala Thr Ser Ser Ser Pro Gln Glu Thr Thr		
290	295	300
Arg Thr Cys Ser Cys Pro Arg Arg Thr Arg Arg Met Phe Arg Trp Ser		
305	310	315
		320
Lys		

&lt;210&gt; 171

&lt;211&gt; 39

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 171

Met Gln Arg Val Glu Val Phe Ser Thr Gln Glu Leu Ala Asp Val Asn
1 5 10 15

Glu Val Leu Arg Met Gly Pro Ser Pro Ile Ser Val Ala Ser Thr Glu
20 25 30

Phe Cys Tyr Pro Ser Phe Arg
35

&lt;210&gt; 172

&lt;211&gt; 193

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 172

Gly Trp Gly His Leu Leu Phe Leu Trp Pro Val Leu Ser Phe Val Ile  
 1 5 10 15

Leu Pro Leu Gly Lys Glu Cys Gln Trp Thr Asp Ala Cys Leu Ser His  
 20 25 30

Pro Cys Ala Asn Gly Ser Thr Cys Thr Thr Val Ala Asn Gln Phe Ser  
 35 40 45

Cys Lys Cys Leu Thr Gly Phe Thr Gly Gln Lys Cys Glu Thr Asp Val  
 50 55 60

Asn Glu Cys Asp Ile Pro Gly His Cys Gln His Gly Gly Thr Cys Leu  
 65 70 75 80

Asn Leu Pro Gly Ser Tyr Gln Cys Gln Cys Leu Gln Gly Phe Thr Gly  
 85 90 95

Gln Tyr Cys Asp Ser Leu Tyr Val Pro Cys Ala Pro Ser Pro Cys Val  
 100 105 110

Asn Gly Gly Thr Cys Arg Gln Thr Gly Asp Phe Thr Phe Glu Cys Asn  
 115 120 125

Cys Leu Pro Gly Lys Glu Leu Pro Ser Val Pro Gly Leu Gly Asp Lys  
 130 135 140

Pro Leu Ala Gln Glu Val Val Gly Val Ala Gln Leu Phe Phe Leu Gly  
 145 150 155 160

Ser Ala Arg Lys Lys Gly Ser Glu Asn Phe Val Gly Gly Gly Leu Leu  
 165 170 175

Val Arg Glu Glu Phe Tyr Gly Pro Thr Val Val His Lys Leu Ser Arg  
 180 185 190

Gly

&lt;210&gt; 173

&lt;211&gt; 72

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 173

Met Pro Ala Cys Leu Ile Pro Val Gln Met Glu Val Pro Val Pro Leu  
 1 5 10 15

Trp Pro Thr Ser Ser Pro Ala Asn Ala Ser Gln Ala Ser Gln Gly Arg  
 20 25 30

Ser Val Arg Leu Met Ser Met Ser Val Thr Phe Gln Asp Leu Pro Ala

35 40 45

Trp Trp His Leu Pro Gln Pro Ala Trp Phe Leu Pro Val Pro Val Pro  
 50 55 60

Ser Gly Leu His Arg Pro Val Leu  
 65 70

<210> 174  
 <211> 73  
 <212> PRT  
 <213> Homo sapiens

<400> 174

Met Leu Arg Ala Gly Ala Ala Gln Thr Cys Ser Ala Gly Leu Gln Val  
 1 5 10 15

Leu Lys Pro Tyr Trp Gly Trp Val Gly Ser Gly Ala Ala Ala Phe Ala  
 20 25 30

Thr Leu Arg Ile Gly Ala Lys Ala Thr Asp Val Tyr Leu Thr Val Thr  
 35 40 45

Leu His Trp Val Leu Lys Glu Ile Ile Ser Arg Cys Asn Tyr Asn Tyr  
 50 55 60

Cys Leu Leu Arg Lys Ile Trp Glu Phe  
 65 70

<210> 175  
 <211> 78  
 <212> PRT  
 <213> Homo sapiens

<400> 175

Met Val Leu Val Ser Ser Phe Phe Val Phe Tyr Ser Val His Ser Phe  
 1 5 10 15

Leu Thr Ile Trp Thr Thr Val Val Ala Asn Pro Gly Gln Trp Ile Val  
 20 25 30

Thr Asn Ser Val Leu Val Ala Ser Cys Phe Pro Ala Arg Ser Pro Phe  
 35 40 45

Val Leu Ile Met Ser Asp Thr His Ile Ser Gln Phe Cys Phe Ala Cys  
 50 55 60

Arg Thr Arg Lys Thr Leu Phe Pro Asn Leu Val Val Met Pro  
 65 70 75

<210> 176  
 <211> 249  
 <212> PRT  
 <213> Homo sapiens

<400> 176

Met Trp Arg Lys Asn Gln Tyr Val Ser Asn Gly Leu Arg Asp Phe Ala

1                      5                      10                      15  
 Glu Arg Gly Glu Ala Trp Ala Leu Met Lys Glu Ile Glu Ala Ala Gly  
                     20                      25                      30  
 Glu Ala Leu Gln Ser Val His Ala Val Phe Ser Ala Pro Ala Val Pro  
                     35                      40                      45  
 Ser Gly Thr Gly Gln Thr Ser Ala Glu Leu Glu Val Gln Arg Arg His  
                     50                      55                      60  
 Ser Leu Val Ser Phe Val Val Arg Ile Val Pro Ser Pro Asp Trp Phe  
                     65                      70                      75                      80  
 Val Gly Val Asp Ser Leu Asp Leu Cys Asp Gly Asp Arg Trp Arg Glu  
                     85                      90                      95  
 Gln Ala Ala Leu Asp Leu Tyr Pro Tyr Asp Ala Gly Thr Asp Ser Gly  
                     100                      105                      110  
 Phe Thr Phe Ser Ser Pro Asn Phe Ala Thr Ile Pro Gln Asp Thr Val  
                     115                      120                      125  
 Thr Glu Ile Thr Ser Ser Ser Pro Ser His Pro Ala Asn Ser Phe Tyr  
                     130                      135                      140  
 Tyr Pro Arg Leu Lys Ala Leu Pro Pro Ile Ala Arg Val Thr Leu Val  
                     145                      150                      155                      160  
 Arg Leu Arg Gln Ser Pro Arg Ala Phe Ile Pro Pro Ala Pro Val Leu  
                     165                      170                      175  
 Pro Ser Arg Asp Asn Glu Ile Val Asp Ser Ala Ser Val Pro Glu Thr  
                     180                      185                      190  
 Pro Leu Asp Cys Glu Val Ser Leu Trp Ser Ser Trp Gly Leu Cys Gly  
                     195                      200                      205  
 Gly His Cys Gly Arg Leu Gly Thr Lys Ser Arg Thr Arg Tyr Val Arg  
                     210                      215                      220  
 Val Gln Pro Ala Asn Asn Gly Ser Pro Cys Pro Glu Leu Glu Glu Glu  
                     225                      230                      235                      240  
 Ala Glu Cys Val Pro Asp Asn Cys Val  
                     245

&lt;210&gt; 177

&lt;211&gt; 191

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 177

Met Ile Thr Val Asp Ile Ile Pro Ser Gly Trp Asn Ser Ala Asp Gly  
 1                      5                      10                      15  
 Lys Ser Asp Lys Thr Lys Ser Ala Pro Ser Arg Asp Pro Glu Arg Leu  
                     20                      25                      30

Gln Lys Ile Lys Glu Ser Leu Leu Leu Glu Asp Ser Glu Glu Glu Glu  
 35 40 45  
 Gly Asp Leu Cys Arg Ile Cys Gln Met Ala Ala Ala Ser Ser Ser Asn  
 50 55 60  
 Leu Leu Ile Glu Pro Cys Lys Cys Thr Gly Ser Leu Gln Tyr Val His  
 65 70 75 80  
 Gln Asp Cys Met Lys Lys Trp Leu Gln Ala Lys Ile Asn Ser Gly Ser  
 85 90 95  
 Ser Leu Glu Ala Val Thr Thr Cys Glu Leu Cys Lys Glu Lys Leu Glu  
 100 105 110  
 Leu Asn Leu Glu Asp Phe Asp Ile His Glu Leu His Arg Ala His Ala  
 115 120 125  
 Asn Glu Gln Ala Glu Tyr Glu Phe Ile Ser Ser Gly Leu Tyr Leu Val  
 130 135 140  
 Val Leu Leu His Leu Cys Glu Gln Ser Phe Ser Asp Met Met Gly Asn  
 145 150 155 160  
 Thr Asn Glu Pro Ser Thr Arg Val Arg Leu Gln Arg Met Ile Pro Lys  
 165 170 175  
 Lys Thr Glu Thr Ile Thr Gly His Leu Ile Leu Pro Asn Phe Ile  
 180 185 190

&lt;210&gt; 178

&lt;211&gt; 80

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 178

Met Phe Leu Ala Cys Leu Cys Leu Glu Asn Trp Ser Ser Gln Ala Pro  
 1 5 10 15  
 Leu Ala Ala Thr Ser Pro Cys Trp Ala Ser Glu Thr Ser Leu Cys Leu  
 20 25 30  
 Val Ser Tyr Tyr Ala Leu Ser Phe Ala Met Thr Thr Thr Lys Ser Lys  
 35 40 45  
 Pro Val Gly Thr Pro Val Gly Pro Leu Asp Leu Pro Thr Ser Pro Gly  
 50 55 60  
 Ala Cys Arg Arg Ser Pro Thr Phe Thr Ala Pro Ser Ser Asp Thr Leu  
 65 70 75 80

&lt;210&gt; 179

&lt;211&gt; 62

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 179

Met Pro Gly Phe Ala Gly Phe Ile Cys Leu Ile Leu Phe Cys Val Phe

1                      5                      10                      15  
 Ser Trp Leu Phe Gly Ser Phe Pro Gly Thr Leu Asp Gly Ser Ile Pro  
                     20                      25                      30  
 Arg His Leu Val Ile Lys Gln Leu Ser Pro Thr Pro Tyr His Gly Lys  
                     35                      40                      45  
 Arg Gly Arg Asn Ile Ala Pro Ser Leu Ile Thr Tyr His Leu  
                     50                      55                      60

<210> 180  
 <211> 61  
 <212> PRT  
 <213> Homo sapiens

<400> 180  
 Met Leu Gly Ser Leu Gly Asp Ala Arg Phe Cys Gly Phe Tyr Leu Phe  
   1                      5                      10                      15  
 Asn Phe Ile Leu Cys Phe Leu Leu Ala Leu Trp Val Phe Pro Gly Tyr  
                     20                      25                      30  
 Thr Arg Trp Leu His Pro Lys Ala Ser Cys His Lys Thr Ala Phe Pro  
                     35                      40                      45  
 His Pro Ile Ser Trp Glu Lys Gly Glu Lys Tyr Ser Pro  
                     50                      55                      60

<210> 181  
 <211> 60  
 <212> PRT  
 <213> Homo sapiens

<400> 181  
 Met Met Ile Ser Leu His Thr Val Gln Ser His Asn Leu Lys Ile Lys  
   1                      5                      10                      15  
 Leu Ser Trp Leu Cys Phe Leu Cys Ser Cys Gln Asn Ile Gly Thr Ile  
                     20                      25                      30  
 Gly Arg Ser Lys Thr Phe Ile Leu Leu Leu Gln Val Tyr Leu Gly Thr  
                     35                      40                      45  
 Phe Thr Cys Val Phe Lys Gly Ile Ser Phe Gln Gln  
                     50                      55                      60

<210> 182  
 <211> 227  
 <212> PRT  
 <213> Homo sapiens

<400> 182  
 Met Met Gly Ser Glu Ala Ala Gly Arg Gly Ser Gln Glu Leu Leu Val  
   1                      5                      10                      15  
 Val Gln Pro Val Leu Pro Ser Glu Ala Leu Leu Phe Pro Gly Leu Pro

20	25	30
Ala Gly Phe Ser Arg Arg Leu Ser Ser Asn Ala Gly Pro Arg Leu Leu 35 40 45		
Ala Trp Val Leu Ala Cys Pro Leu Arg Pro Leu Ala Ala Cys Leu Leu 50 55 60		
Ser Leu Val Ala Leu Pro Gly Cys Trp Ala Ala Leu Ser Gly Arg Leu 65 70 75 80		
Leu Pro Val Cys Phe Pro Trp Trp Leu Cys Leu Gly Ala Gly Pro Ala 85 90 95		
Phe Ser Gly Cys Leu Leu Pro Val Tyr Cys His Leu Gln Arg Gly Ser 100 105 110		
Leu Leu Arg Pro Thr Leu Leu His Leu Ala Pro Pro Trp Leu Leu Ala 115 120 125		
Trp Pro Asn Leu Ala Phe Cys Ala Met Leu Glu Leu Glu Leu Leu Leu 130 135 140		
Phe Phe Arg Gly Gly Asn Arg Val Glu Ser Gly Lys Gly Leu Ala Pro 145 150 155 160		
Lys Cys Cys Cys Cys Gly Phe Phe Ala Phe Ser Lys Asp Ala Leu Pro 165 170 175		
Gly Pro Lys Leu Gln Thr Ala Val Leu Ser Lys Gln Val Arg Ser Leu 180 185 190		
Gly Phe Gly Ala His Leu Leu Ser Gly Ser Ile Ser Ile Leu Leu Leu 195 200 205		
Ala Thr Ser Gly Gln Arg Pro Pro Gln Pro His Ile Ala Arg Cys Trp 210 215 220		
Gln Lys Gly 225		

&lt;210&gt; 183

&lt;211&gt; 97

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 183

Met Leu Ser Cys Thr Leu Gly Leu Thr Val Cys Pro Leu Ser Pro Ala 1 5 10 15
Pro Ser Val Thr Leu Ala Val Ala Leu Asn Gly Gln Leu Arg Arg Pro 20 25 30
Leu Cys Cys Ser Ser Ala Phe Pro Glu Val Gly Glu Pro Ala Trp Pro 35 40 45
Arg Pro Leu Ser Ser Asp Gln Ala Leu Ser Pro Arg Ser Tyr Gly Arg 50 55 60

Pro Gly Ser Gly Val Gly Thr His Gly Pro Gly Trp Gly Gly Ala Gln  
 65 70 75 80

Ser Asp Val Asn Phe Phe Pro Cys Val Asp Met Tyr Ser Gln Arg Val  
 85 90 95

Val

<210> 184  
 <211> 68  
 <212> PRT  
 <213> Homo sapiens

<400> 184  
 Met Cys Phe Leu Leu Phe Gly Ser Leu Cys Ile Tyr Tyr Phe Ser Leu  
 1 5 10 15

Phe Leu Val Phe Phe Phe Ser Cys Phe Cys Phe Val Trp Cys Phe Val  
 20 25 30

Pro Val Phe Ile Val Ser Gly Ile Ser Leu Pro Leu Trp Ile Pro His  
 35 40 45

Gly Leu Asp Arg Asp Gly Pro Val Met Pro Ser Ser Phe Leu Leu Leu  
 50 55 60

Leu Leu Leu Trp  
 65

<210> 185  
 <211> 142  
 <212> PRT  
 <213> Homo sapiens

<400> 185  
 Met Phe Ser Cys Asn Glu Asn Ser Ile Phe Phe Arg Ile Gly Phe Val  
 1 5 10 15

Phe Ile Leu Leu Ser Phe Ile Ser Ser Cys Gln Thr Leu Asn Gly Tyr  
 20 25 30

Val Cys Ile Leu Ile Thr Leu Phe Ser Leu Leu Trp Lys Arg Arg Thr  
 35 40 45

Arg Glu Gln Met Leu Leu Arg Ala Gly Val Ser Glu Lys Asn Leu Ser  
 50 55 60

Met Leu Phe Asn Val Phe Leu Pro Leu Pro His Ser Val Cys Val Thr  
 65 70 75 80

Phe Tyr Asn Ile Lys Lys Tyr Tyr Asn Ile Ser Arg Ile Trp Asn Cys  
 85 90 95

His His Asp Glu Trp Pro Phe Gln Cys Ile Val Thr Glu Ile Pro Glu  
 100 105 110

Asp Ser Pro Gly Leu Gln Phe His Trp Phe Leu Leu Gln Phe Leu Val



115                      120                      125

Ala Val Ile Val Ala Val Ser Ser Leu Lys Asp Leu Leu Trp  
 130                      135                      140

<210> 186  
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 <212> PRT  
 <213> Homo sapiens

<400> 186  
 Met Ser Cys Pro Leu Pro Leu Leu Ile Ser Ala Ile Ala Ala Val Gly  
 1                      5                      10                      15

Ser Ser Met Gln Thr His Ala Arg Ala Ser Phe Ala Ala Gly Pro Ser  
                     20                      25                      30

Gln Glu Asp Phe Ser Ala His Leu Ala Gln Asp Gln His Ser Pro Glu  
                     35                      40                      45

Val Gln Gly His Tyr His Ala Arg Gly Asn Pro Pro Ala Val Gly Asp  
                     50                      55                      60

Thr Ser Leu Trp Met Lys Val Pro Thr Ser His His Ser Asp Glu Lys  
                     65                      70                      75                      80

His Gln Glu Ala Ser Cys Thr Phe Leu Lys Arg Pro Gln Gln Asp Gln  
                     85                      90                      95

Ser Pro Ile Ala His Ser Ser His Leu Asn Asn Ala Pro Phe Tyr  
                     100                      105                      110

<210> 187  
 <211> 72  
 <212> PRT  
 <213> Homo sapiens

<400> 187  
 Met Phe Gly Met Pro His Thr Met Ser Cys Pro Leu Pro Leu Leu Ile  
 1                      5                      10                      15

Ser Ala Ile Ala Ala Val Gly Ser Ser Met Gln Thr His Ala Arg Ala  
                     20                      25                      30

Ser Phe Ala Ala Gly Pro Ser Gln Lys Thr Ser Gln Pro Ile Trp Ser  
                     35                      40                      45

Arg Ile Phe Leu Pro Leu Lys Val Thr Ala Pro Lys Ser Cys Pro Met  
                     50                      55                      60

Phe Tyr Phe Gln Glu Phe Pro Asn  
                     65                      70

<210> 188  
 <211> 109  
 <212> PRT  
 <213> Homo sapiens

&lt;400&gt; 188

Met Asp Ala Arg Trp Trp Ala Val Val Val Leu Ala Ala Phe Pro Ser  
 1 5 10 15

Leu Gly Ala Gly Gly Glu Thr Pro Glu Ala Pro Pro Glu Ser Trp Thr  
 20 25 30

Gln Leu Trp Phe Phe Arg Phe Val Val Asn Ala Ala Gly Tyr Ala Ser  
 35 40 45

Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Phe Arg Arg Lys Asn  
 50 55 60

Tyr Leu Glu Thr Gly Met Gly Leu Cys Phe Pro Leu Val Lys Ala Cys  
 65 70 75 80

Val Phe Gly Asn Glu Pro Lys Ala Ser Asp Glu Val Pro Leu Arg Pro  
 85 90 95

Gln Gln Arg Arg Gln Arg Pro Pro Arg Cys Gly Arg Pro  
 100 105

&lt;210&gt; 189

&lt;211&gt; 76

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 189

Met Trp Pro Ala Leu His Leu Leu His His Trp Ala Val Trp Gly Cys  
 1 5 10 15

Arg Leu His His His His Asp Pro Pro Pro Gly Leu Cys His Pro Ser  
 20 25 30

Phe Leu Pro Ser Leu Trp Pro His Cys His Cys Gly Gly Arg Ala Gly  
 35 40 45

Gly Gly Cys Gly Leu Cys Cys Pro Pro Ala Gln Ser Leu Arg Ala Gly  
 50 55 60

Pro Ser Lys Ala Thr Gly Lys Glu Gly Cys Ala Cys  
 65 70 75

&lt;210&gt; 190

&lt;211&gt; 168

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 190

Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro Lys Gly  
 1 5 10 15

Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro Leu Val  
 20 25 30

Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val Ile Leu  
 35 40 45

Leu Asp Thr..Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys Arg Leu  
 50 55 60  
 Val Leu Arg Cys Ser Met Asp Asp Ser Ala Gly Pro Arg Glu Trp Leu  
 65 70 75 80  
 Pro Arg Asp Ser Glu Cys His Leu Cys Met Ser Val Thr Thr Gln Ala  
 85 90 95  
 Gly Asn Ser Ser Glu Gln Ala Ile Pro Gln Ala Met Leu Gln Ala Cys  
 100 105 110  
 Val Gly Ser Trp Leu Asp Arg Glu Lys Cys Lys Gln Phe Val Glu Gln  
 115 120 125  
 His Thr Pro Gln Leu Leu Thr Leu Val Pro Arg Gly Trp Asp Ala His  
 130 135 140  
 Thr Thr Cys Gln Ala Leu Gly Val Cys Gly Thr Met Ser Ser Pro Leu  
 145 150 155 160  
 Gln Cys Ile His Ser Pro Asp Leu  
 165

<210> 191  
 <211> 272  
 <212> PRT  
 <213> Homo sapiens

<400> 191  
 Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Leu Pro Thr  
 1 5 10 15  
 Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys  
 20 25 30  
 Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln  
 35 40 45  
 Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly  
 50 55 60  
 Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn  
 65 70 75 80  
 Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Leu Ser Glu Gln Gln Phe  
 85 90 95  
 Pro Ile Pro Leu Pro Tyr Cys Trp Leu Cys Arg Ala Leu Ile Lys Arg  
 100 105 110  
 Ile Gln Ala Met Ile Pro Lys Gly Ala Leu Ala Val Ala Val Ala Gln  
 115 120 125  
 Val Cys Arg Val Val Pro Leu Val Ala Gly Gly Ile Cys Gln Cys Leu  
 130 135 140  
 Ala Glu Arg Tyr Ser Val Ile Leu Leu Asp Thr Leu Leu Gly Arg Met

145                      150                      155                      160  
 Leu Pro Gln Leu Val Cys Arg Leu Val Leu Arg Cys Ser Met Asp Asp  
                                  165                      170                      175  
 Ser Ala Gly Pro Arg Glu Trp Leu Pro Arg Asp Ser Glu Cys His Leu  
                                  180                      185                      190  
 Cys Met Ser Val Thr Thr Gln Ala Gly Asn Ser Ser Glu Gln Ala Ile  
                                  195                      200                      205  
 Pro Gln Ala Met Leu Gln Ala Cys Val Gly Ser Trp Leu Asp Arg Glu  
                                  210                      215                      220  
 Lys Cys Lys Gln Phe Val Glu Gln His Thr Pro Gln Leu Leu Thr Leu  
 225                                   230                      235                      240  
 Val Pro Arg Gly Trp Asp Ala His Thr Thr Cys Gln Ala Leu Gly Val  
                                  245                      250                      255  
 Cys Gly Thr Met Ser Ser Pro Leu Gln Cys Ile His Ser Pro Asp Leu  
                                  260                      265                      270

<210> 192  
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 <212> PRT  
 <213> Homo sapiens

<400> 192  
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   1                                 5                                 10                                 15  
 Leu Leu Pro Arg Leu Glu Cys Ser Ser Thr Ile Ser Ala Leu Thr Ala  
                                  20                                 25                                 30  
 Thr Ser Val Ser Trp Val Gln Ala Ile Leu Leu Pro Gln Pro Pro Lys  
                                  35                                 40                                 45  
 Tyr Leu Gly Leu Gln Ala Cys Ala Thr Thr Pro Gly  
   50                                 55                                 60

<210> 193  
 <211> 357  
 <212> PRT  
 <213> Homo sapiens

<400> 193  
 Met Pro Ile Leu Thr Gly Asp Phe Leu Leu Pro Thr Pro Gln Phe Tyr  
   1                                 5                                 10                                 15  
 Ala Glu Asn Ile Asn Thr Thr Ser Leu Thr Cys Ser Ser Asp Arg Met  
                                  20                                 25                                 30  
 Arg Val Ile Ile Ser Lys Ser Tyr Leu Glu Ala Phe Asn Ser Asn Gly  
                                  35                                 40                                 45  
 Asn Asn Leu Gln Leu Lys Asp Pro Thr Cys Arg Pro Lys Leu Ser Asn  
   50                                 55                                 60

Val Val Glu Phe Ser Val Pro Leu Asn Gly Cys Gly Thr Ile Arg Lys  
 65 70 75 80  
 Val Glu Asp Gln Ser Ile Thr Tyr Thr Asn Ile Ile Thr Phe Ser Ala  
 85 90 95  
 Ser Ser Thr Ser Glu Val Ile Thr Arg Gln Lys Gln Leu Gln Ile Ile  
 100 105 110  
 Val Lys Cys Glu Met Gly His Asn Ser Thr Val Glu Ile Ile Tyr Ile  
 115 120 125  
 Thr Glu Asp Asp Val Ile Gln Ser Gln Asn Ala Leu Gly Lys Tyr Asn  
 130 135 140  
 Thr Ser Met Ala Leu Phe Glu Ser Asn Ser Phe Glu Lys Thr Ile Leu  
 145 150 155 160  
 Glu Ser Pro Tyr Tyr Val Asp Leu Asn Gln Thr Leu Phe Val Gln Val  
 165 170 175  
 Ser Leu His Thr Ser Asp Pro Asn Leu Val Val Phe Leu Asp Thr Cys  
 180 185 190  
 Arg Ala Ser Pro Thr Ser Asp Phe Ala Ser Pro Thr Tyr Asp Leu Ile  
 195 200 205  
 Lys Ser Gly Cys Ser Arg Asp Glu Thr Cys Lys Val Tyr Pro Leu Phe  
 210 215 220  
 Gly His Tyr Gly Arg Phe Gln Phe Asn Ala Phe Lys Phe Leu Arg Ser  
 225 230 235 240  
 Met Ser Ser Val Tyr Leu Gln Cys Lys Val Leu Ile Cys Asp Ser Ser  
 245 250 255  
 Asp His Gln Ser Arg Cys Asn Gln Gly Cys Val Ser Arg Ser Lys Arg  
 260 265 270  
 Asp Ile Ser Ser Tyr Lys Trp Lys Thr Asp Ser Ile Ile Gly Pro Ile  
 275 280 285  
 Arg Leu Lys Arg Asp Arg Ser Ala Ser Gly Asn Ser Gly Phe Gln His  
 290 295 300  
 Glu Thr His Ala Glu Glu Thr Pro Asn Gln Pro Phe Asn Ser Val His  
 305 310 315 320  
 Leu Phe Ser Phe Met Val Leu Ala Leu Asn Val Val Thr Val Ala Thr  
 325 330 335  
 Ile Thr Val Arg His Phe Val Asn Gln Arg Ala Asp Tyr Lys Tyr Gln  
 340 345 350  
 Lys Leu Gln Asn Tyr  
 355

&lt;210&gt; 194

&lt;211&gt; 169

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 194

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Met Gln Cys Leu Leu Pro Tyr Gln Ser Lys Glu Pro Ser Cys Leu Pro
 1             5             10             15

Pro Leu Pro Leu Asn Leu Pro Leu Pro Pro Cys Leu Cys Pro Leu Leu
      20             25             30

Gln Leu Asn Ala Ala Met Thr Arg Lys Glu Lys Thr Lys Glu Gly Gln
      35             40             45

Arg Ala Ala Gln Phe Ser Ala Gly Ala Asp Ala Gly Ser Gly Gly Gly
      50             55             60

Leu Ser Arg Gln Lys Asp Thr Lys Arg Pro Met Leu Leu Val Ile His
      65             70             75             80

Asp Val Val Leu Glu Leu Leu Thr Ser Ser Asp Cys His Ala Asn Pro
      85             90             95

Arg Lys Tyr Pro Thr Cys Gln Lys Ser Glu Val Leu Gly Val Ser Ile
      100            105            110

Tyr Val Ser Ile Cys Pro Ser Thr Arg Pro Arg Asp Lys Asn Lys Thr
      115            120            125

Lys Lys Arg Cys Gln Val Leu Glu Ala Val Leu Val Ser Lys Pro Ser
      130            135            140

Gly Ser Cys His Gln Gly Ser Phe Glu Ile Val Pro His Val Lys Gly
      145            150            155            160

Asn Leu Ala Phe Thr Ser Ser Asn Asn
      165

```

## INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US00/07285

**A. CLASSIFICATION OF SUBJECT MATTER**

IPC(7) : C12Q 1/68; C12N 15/00, 15/09, 15/63, 15/86

US CL : 435/6, 69.1, 69.3, 320.1, 455, 471; 530/300, 350; 424/189.1

According to International Patent Classification (IPC) or to both national classification and IPC

**B. FIELDS SEARCHED**

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/6, 69.1, 69.3, 320.1, 455, 471; 530/300, 350; 424/189.1

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

EAST, USPATFULL

**C. DOCUMENTS CONSIDERED TO BE RELEVANT**

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X -- Y	Database EST on STN. Hudson et al. AN X11582. 'New isolated nucleic acid segments from the human genome - used for determining polymorphic forms for use in e.g. forensics, paternity testing or phenotypic typing for disease' WO 98/20165 see, bases 1-67, which would hybridize to SEQ ID NO: 1.	1 -- 2-11
X -- Y	Database EST on STN. Hillier et al. AN W51776. 'The WashU-Merck EST Project' 11 October 1996. See Sequence Alignment (attached) disclosing 85% similarity to SEQ ID NO: 1, and would hybridize to SEQ ID NO: 1	1 -- 2-11
X -- Y	Database EST on STN. 'NCI-CGAP' AN AA568724. '09 September 1997. See Sequence Alignment (attached) which discloses a polynucleotide with 88% similarity to SEQ ID NO: 1 and would hybridize to SEQ ID NO: 1.	1 -- 2-11

☒ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

* Special categories of cited documents:	*T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
*A* document defining the general state of the art which is not considered to be of particular relevance	*X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
*E* earlier document published on or after the international filing date	*Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
*L* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	*A* document member of the same patent family
*Q* document referring to an oral disclosure, use, exhibition or other means	
*P* document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search

27 JUNE 2000

Date of mailing of the international search report

19 JUL 2000

Name and mailing address of the ISA/US  
Commissioner of Patents and Trademarks  
Box PCT  
Washington, D.C. 20231

Facsimile No. (703) 305-3230

Authorized officer

MARY K ZEMAN

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## INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US00/07285

## C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X, P --- Y, P	Database Gen EMBL. AN AC009651. Birren et al. 'Homo sapiens chromosome 11, clone' 29 September 1999. See Sequence Alignment (attached) which discloses a polynucleotide having up to 98% identity to SEQ ID NO: 1, and could encode SEQ ID NO: 2.	1 -- 2-11



# INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US00/07285

## Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:
  
2. ☐ Claims Nos.:  
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
  
3. ☐ Claims Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

## Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

Please See Extra Sheet.

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
  
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:  
1-11, SEQ ID NO: 1 and 2

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.  
☐ No protest accompanied the payment of additional search fees.

# INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US00/07285

## BOX II. OBSERVATIONS WHERE UNITY OF INVENTION WAS LACKING

This ISA found multiple inventions as follows:

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional search fees must be paid.

- Group I, claim(s)1-11, drawn to polynucleotides (SEQ ID NO: 1) and encoded polypeptides (SEQ ID NO: 2), and methods of making the recombinant polypeptides.
- Group II, claim(s) 12-13, drawn to polynucleotides (SEQ ID NO: 3) and encoded polypeptides (SEQ ID NO: 4).
- Group III, claim(s) 14-15, drawn to polynucleotides (SEQ ID NO: 5) and encoded polypeptides (SEQ ID NO: 6).
- Group IV, claim(s)16-17, drawn to polynucleotides (SEQ ID NO: 7) and encoded polypeptides (SEQ ID NO: 8).
- Group V, claim(s) 18-19, drawn to polynucleotides (SEQ ID NO: 9) and encoded polypeptides (SEQ ID NO: 10).
- Group VI, claim(s) 20-21, drawn to polynucleotides (SEQ ID NO: 11) and encoded polypeptides (SEQ ID NO: 12).
- Group VII, claim(s)22-23, drawn to polynucleotides (SEQ ID NO: 13) and encoded polypeptides (SEQ ID NO: 14).
- Group VIII, claim(s) 24-25, drawn to polynucleotides (SEQ ID NO: 15) and encoded polypeptides (SEQ ID NO: 16).
- Group IX, claim(s) 26-27, drawn to polynucleotides (SEQ ID NO: 17) and encoded polypeptides (SEQ ID NO: 18).
- Group X, claim(s)28-29, drawn to polynucleotides (SEQ ID NO: 19) and encoded polypeptides (SEQ ID NO: 20).
- Group XI, claim(s)30-31, drawn to polynucleotides (SEQ ID NO: 21) and encoded polypeptides (SEQ ID NO: 22).
- Group XII, claim(s) 32-33, drawn to polynucleotides (SEQ ID NO: 23) and encoded polypeptides (SEQ ID NO: 24).
- Group XIII, claim(s) 34-35, drawn to polynucleotides (SEQ ID NO: 25) and encoded polypeptides (SEQ ID NO: 26).
- Group XIV, claim(s) 36-37, drawn to polynucleotides (SEQ ID NO: 27) and encoded polypeptides (SEQ ID NO: 28).
- Group XV, claim(s) 38-39, drawn to polynucleotides (SEQ ID NO: 29) and encoded polypeptides (SEQ ID NO: 30).
- Group XVI, claim(s) 40-41, drawn to polynucleotides (SEQ ID NO: 31) and encoded polypeptides (SEQ ID NO: 32).
- Group XVII, claim(s)42-43, drawn to polynucleotides (SEQ ID NO: 33) and encoded polypeptides (SEQ ID NO: 34).
- Group XVIII, claim(s) 44-45, drawn to polynucleotides (SEQ ID NO: 35) and encoded polypeptides (SEQ ID NO: 36).
- Group XIX, claim(s) 46-47, drawn to polynucleotides (SEQ ID NO: 37) and encoded polypeptides (SEQ ID NO: 38).
- Group XX, claim(s) 48-49, drawn to polynucleotides (SEQ ID NO: 39) and encoded polypeptides (SEQ ID NO: 40).
- Group XXI, claim(s)50-51, drawn to polynucleotides (SEQ ID NO: 41) and encoded polypeptides (SEQ ID NO: 42).
- Group XXII, claim(s) 52-53, drawn to polynucleotides (SEQ ID NO: 43) and encoded polypeptides (SEQ ID NO: 44).
- Group XXIII, claim(s) 54-55, drawn to polynucleotides (SEQ ID NO: 45) and encoded polypeptides (SEQ ID NO: 46).
- Group XXIV, claim(s)56-57, drawn to polynucleotides (SEQ ID NO: 47) and encoded polypeptides (SEQ ID NO: 48).
- Group XXV, claim(s) 58-59, drawn to polynucleotides (SEQ ID NO: 49) and encoded polypeptides (SEQ ID NO: 50).
- Group XXVI, claim(s) 60-61, drawn to polynucleotides (SEQ ID NO: 51) and encoded polypeptides (SEQ ID NO: 52).
- Group XXVII, claim(s)62-63, drawn to polynucleotides (SEQ ID NO: 53) and encoded polypeptides (SEQ ID NO: 54).
- Group XXVIII, claim(s) 64-65, drawn to polynucleotides (SEQ ID NO: 55) and encoded polypeptides (SEQ ID NO: 56).
- Group XXIX, claim(s) 66-67, drawn to polynucleotides (SEQ ID NO: 57) and encoded polypeptides (SEQ ID NO: 58).
- Group XXX, claim(s)68-69, drawn to polynucleotides (SEQ ID NO: 59) and encoded polypeptides (SEQ ID NO: 60).
- Group XXXI, claim(s)70-71, drawn to polynucleotides (SEQ ID NO: 61) and encoded polypeptides (SEQ ID NO: 62).
- Group XXXII, claim(s) 72-73, drawn to polynucleotides (SEQ ID NO: 63) and encoded polypeptides (SEQ ID NO: 64).
- Group XXXIII, claim(s) 74-75, drawn to polynucleotides (SEQ ID NO: 65) and encoded polypeptides (SEQ ID NO: 66).
- Group XXXIV, claim(s) 76-77, drawn to polynucleotides (SEQ ID NO: 67) and encoded polypeptides (SEQ ID NO: 68).
- Group XXXV, claim(s) 78-79, drawn to polynucleotides (SEQ ID NO: 69) and encoded polypeptides (SEQ ID NO: 70).
- Group XXXVI, claim(s) 80-81, drawn to polynucleotides (SEQ ID NO: 71) and encoded polypeptides (SEQ ID NO: 72).
- Group XXXVII, claim(s)82-83, drawn to polynucleotides (SEQ ID NO: 73) and encoded polypeptides (SEQ ID NO: 74).
- Group XXXVIII, claim(s) 84-85, drawn to polynucleotides (SEQ ID NO: 75) and encoded polypeptides (SEQ ID NO: 76).
- Group XXXIX, claim(s) 86-87, drawn to polynucleotides (SEQ ID NO: 77) and encoded polypeptides (SEQ ID NO: 78).
- Group XXXX, claim(s) 88-89, drawn to polynucleotides (SEQ ID NO: 79) and encoded polypeptides (SEQ ID NO: 80).
- Group XXXXI, claim(s)90-91, drawn to polynucleotides (SEQ ID NO: 81) and encoded polypeptides (SEQ ID NO: 82).
- Group XXXXII, claim(s) 92-93, drawn to polynucleotides (SEQ ID NO: 83) and encoded polypeptides (SEQ ID NO: 84).
- Group XXXXIII, claim(s) 94-95, drawn to polynucleotides (SEQ ID NO: 85) and encoded polypeptides (SEQ ID NO: 86).

## INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US00/07285

86).

Group XXXXIV, claim(s) 96-97, drawn to polynucleotides (SEQ ID NO: 87) and encoded polypeptides (SEQ ID NO: 88).

Group XXXXV, claim(s) 98-99, drawn to polynucleotides (SEQ ID NO: 89) and encoded polypeptides (SEQ ID NO: 90).

Group XXXXVI, claim(s) 100-101, drawn to polynucleotides (SEQ ID NO: 91) and encoded polypeptides (SEQ ID NO: 92).

Group XXXXVII, claim(s) 102-103, drawn to polynucleotides (SEQ ID NO: 93) and encoded polypeptides (SEQ ID NO: 94).

Group XXXXVIII, claim(s) 104-105, drawn to polynucleotides (SEQ ID NO: 95) and encoded polypeptides (SEQ ID NO: 96).

Group XXXXIX, claim(s) 106-107, drawn to polynucleotides (SEQ ID NO: 97) and encoded polypeptides (SEQ ID NO: 98).

Group L, claim(s) 108-109, drawn to polynucleotides (SEQ ID NO: 99) and encoded polypeptides (SEQ ID NO: 100).

Group LI, claim(s) 101-111, drawn to polynucleotides (SEQ ID NO: 101) and encoded polypeptides (SEQ ID NO: 102).

Group LII, claim(s) 112-113, drawn to polynucleotides (SEQ ID NO: 103) and encoded polypeptides (SEQ ID NO: 104).

Group LIII, claim(s) 114-115, drawn to polynucleotides (SEQ ID NO: 105) and encoded polypeptides (SEQ ID NO: 106).

Group LIV, claim(s) 116-117, drawn to polynucleotides (SEQ ID NO: 107) and encoded polypeptides (SEQ ID NO: 108).

Group LV, claim(s) 118-119, drawn to polynucleotides (SEQ ID NO: 109) and encoded polypeptides (SEQ ID NO: 110).

Group LVI, claim(s) 120-121, drawn to polynucleotides (SEQ ID NO: 111) and encoded polypeptides (SEQ ID NO: 112).

Group LVII, claim(s) 122-123, drawn to polynucleotides (SEQ ID NO: 113) and encoded polypeptides (SEQ ID NO: 114).

Group LVIII, claim(s) 124-125, drawn to polynucleotides (SEQ ID NO: 115) and encoded polypeptides (SEQ ID NO: 116).

Group LIX, claim(s) 126-127, drawn to polynucleotides (SEQ ID NO: 117) and encoded polypeptides (SEQ ID NO: 118).

The inventions listed as Groups ONE (I) to FIFTY NINE (LIX) do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: Each polynucleotide and corresponding polypeptide do not share any sequence homology, similar structure or other feature which could be considered a special technical feature. Each polynucleotide sequence and corresponding polypeptide sequence is a separate and distinct invention, having no obvious shared features, and thus, lack unity under PCT Rule 13.2.

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